SSAATSSSSYPPQL/VYGDNYSNFGVCYGSNPNGGIYSHMSVMPLRSDGSLCLMEALNR SSHSNHHQDSSPKVEDPFYGTHHNNTSHKEAMDLSLDSLFXNTTHEPNTTTNYGEFFSF PQTRANHEEDTRNYGNDPSLTHGGSPRVGVYGEFQQSLSLSMSPRSSCSSGITGGSHHQQ NQNQNHQSQNHQQISEALVETSVGFETTTMAAAKKKRGQEDVVVVGQXQIVHRKSIDT

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REFERENCE
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AUTHORS
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ATU41339
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ORGANISM
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                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                 source
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Arabidopsis thaliana ANT (AINTEGUMENTA) mRNA, complete Cds.
U41339 GI:1244707
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1905)
Elliott.R.C., Betzner,A.S., Huttner,E., Oakes,M.P., Tucker,W.Q.,
Gerentes,D., Perez,P. and Smyth,D.R.
AINTEGUMENTA, an APETALA2-like gene of Arabidopsis with pleiotropic roles in ovule development and floral organ growth
Plant Cell 8 (2), 155-168 (1996)
                                                                                                                                                                                                                                                                                                        Direct Submission
Direct Submission
Submitted (27-NOV-1995) David Smyth, Genetics and Dev. Biology,
Monash University, Wellington Road, Clayton, VIC 3168, Australia
Location/Qualifiers
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8742707
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                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 1905)
                                                                                       /note="similar to APETALA2 protein encoded by GenBank Accession Number Ul2546"
                                                                                                                                                                          /map="between spt and cer-9"
/tissue_type="flower; ovule"
1. .1905
                                                                                                                                                                                                                             /organism="Arabidopsis thaliana"

|mol type="mmNNA"

/strain="Landsberg erecta"

/db_xref="taxon:3702"

/chromosome="4"
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                                                        product = "ANT
                                                                        codon_start=1
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Percent Similarity:
Best Local Similarity:
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US-10-024-632-2 (1-663) x ATU41339 (1-1905)
                                                             Query Match:
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                                                                                                                                                                      Alignment Scores:
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/note="encodes first AP2 domain"
1184. .1391
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AALKYWGPSTHTNISALBNYQKEIEDMKMMTRQBYVAHLÆRKSSGFSRGASIYRGVTRH
HQHGRWQARIGRVAGNKDLYLGTFGTQBEAARAYDVAALKFRGTNAVTNFDITRYDVD
RIMSSNTLLGGELAKRNNNSIVVRNTEDQTALNAVVBGGSNKEVSTPERILLSFPAIFA
LPQVNQKMFGSNMGGNMSFWTSNFNAELKTVALTLFQMFVFAAWADS"
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/note="ecodes second AP2 domain"
                                                           6.66e-81
1328.00
52.84*
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37.92*
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Matches:
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217	198 GlybeubysAsnTrpValAlaProThrArgGluPheSerThrHisGlnGlnValLeuGlu 217	191	¥
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53 5	ACTACAAACTTTCAAGAGTTCTTTAGCTTCCCTCAAACCAGAAACCAT 535	488	Ď.
157	AspLeuLeuSerGlnProPheArgGlnGlnGlyHisMetSerValGln	142	¥
487	437 GATCTTAGCTTAGATAGTTTATTCTACAACACCACTCATGAGCCCAACACG 487	43	Ŗ.
141	LeuSerLeuAspSerIleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArg	12:	¥
436		389	Ъ
122	AspPheLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGluArgGly 122	104	¥
388	GAAGCTCTCAACAGATCTTCTCACTCGAATCACCATCAAGATTCATCTCCAAAGGTGGAG 388	329	β.
103		84	¥
328	GGAATCTATTCTCACATGTCTGTGATGCCACTCAGATCTGATGGTTCTCTTTGCTTAATG	269	ğ
83	AsnPheHisSerProLeuThrValMetProLeuLysSerAspGlySerLeuCysIleLeu	64	¥
268	GGTGACAACACTAGCAACTTTGGTGTTTGCTATGGATCTAACCCAAATGGA 268	218	ğ
63		44	¥
217	TCATCTTCAACTTCTTCAGCTGCAACTTCTTCTTCTTCTTCTTCCACCTCAACTTGTTGTT 217	158	Ŗ.
43		30	¥
157	TTCTCATTGTCTTCAAATATGATGAAAATGGGGAGGTAGAGGAGGTAGAGAAGCTATTTAC 157	98	ğ
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N;Alternate names: AP2 domain-containing protein; protein T28I19.30
C;Bpecies: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 22-Oct-1999
C;Accession: S71365; T06022
R;Klucher, K.
submitted to the EMBL Data Library, November 1995
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A;Accession: T06022
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-555 <BEV'
A;Cross-references: EMBL:AL035709; GSPDB:GN00062; ATSP:T28I19.30
A;Experimental source: cultivar Columbia; BAC clone T28I19
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                                                                                                                                                                                                                                                                                                                                                                                                                      MKSFCDNDDNNHSNTTNLLGFSLSSNMMKMGGRGGREAIYSSSTSSAATSSSSVPPQLVV
                                                                                                                                                                                   THPYYSGLACHGLYQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLE
                                                                                       QQMNCGMGNERNGVSLGSVGCGEL-QSLSLSMSPGSQSSCVTAPS---
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                                                       -----GSFNVGV-----YGEFQQSLSLSMSPGSQSSCITGSHHHQQNQNQNHQSQNH
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C;Accession: B96750
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Ression: B96750
A;Ression: B96750
A;Ressidues: 1-425 <870>
A;Ressidues: GB;AE005173; NID:96648171; PIDN:AAF21171.1; GSPDB:GN00141
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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Best Local Similarity 43.4%;
Matches 214; Conservative 6
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                                    132 SQNABAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETTKETHVSDCSSL
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                                                                                                                                                     WLGFSLTPPLRICNSEEEELRHDGSDGTLFF-----
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; Pred. No. 1.5e-57;
60; Mismatches 108;
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A;Map position: 5
A;Introns: 78/1; 216/2; 244/1; 273/3; 298/2; 315/2; 341/1
A;Note: T10B6_90
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A;Molecule type: DNA
A;Residues: 1-581 <SAT>
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A;Accession: T51580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ovule development protein aintegumenta-like protein - Arabidopsis thaliana N,Alternate names: protein T1086 90 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000 C;Accession: T51580
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A;Experimental source: cultivar Columbia; BAC clone T10B6
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Best Local S
Matches 255
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Sines 255;
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                                                           147
                                                                                                235
                                                                                                                                                                                                                                                     127
                      290 DTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDL
                                                                                                                                                                             187
                                                                                                                                                                                                                  88
                                                                                                                                                                                                                                                                                            35
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                                                                                                                                                                                                                                                                                                                                76
                                                                                                                                                                                                                                                                                                                                                                                                        16 HNWLGFSLSPHMKWEATSAATVPTTFYMSPSQSHLSNFGMCYGVGENGNFHSPLTVMPLK 75
                                                                                                                                                                                                                                                                                                                                                                     v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLAALKYWGPTTHLNFPLSNYEKEIBELNNMNRQEFVAMLRRNGSGFSRGASVYRGVTRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIDTFGORTSOYRGVTRHRWTGRYEAHLWDNSCKXEGOTRKGROVYLGGYDMEEKAARAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGSM-----LSLALSHGACSDLINESNVSARVEEPVKVDEKRKRLVVKPQVKESVPRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPNLSNDYGGFERVGSVSVFKSWLEQGTPAFPLSSHYVTEEAGTSNNISHFSNEETGYNT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPOMTEG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVDSYGQRTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRRGRQAKIGGYDEEEKAARAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GSVGCGELOSLSLSMSPGSQSSCVTAPSGT----DSVAVDAK-KRGHAKLGQKQPVHRK
                                                                                                                                                                                                                                                       SIYYNSQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETTKETHVS 186
                                                                                                                                                                                                                                                                                                                                SDGSLCI-LEALKRSQTQVMVPTSSP---KLEDFLGGATMGTHEYGSHER-----GLSLD 126
                                                                                                                                                                                                                                                                                                                                                                       NNWLGFSLSPH----
                                                         DCSSIMPQMTEGIKNWVAPTRE-FSTHQQVIEQQMNCGMGNERNGVSIG------
                                                                                                                                                                                                                                                                                            VAGGYCFDLAAPSDESSAVQTSFLSPFGVTLEAF----TRDNNSHSRDWDINGGACN
                                                                                                                                        -----PK----LENFLGRTTTIYNTNETVVDGNGDCGGGDGGGGGSLGLSMIKTWLSNH 146
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             26.2%; Score 916.5; DB 2; 35.2%; Pred. No. 7.5e-57; tive 76; Mismatches 170;
                                                                                                --SISISMSPGSQSSCVTAPSGTDSVAVDAKKRGHAKLGQKQPVHRKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---LKNWV---APTREFSTHQQVLEQQMNCGM---GNERNGVSL
                                                                                                                                                                                                                                                                                                                                                                       -----HRTDVDSSTTRTAVD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 581;
                          349
                                                                                                  289
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Qy 470 SSMLLAGILARENCONDEPNNOIDNESSYTEMPRETOVORAGE-INMINISHMONT, 527 pb 575 FFSIPTGSSKARLOG  QY 528 FNIBS	202 ESFGORTSIYRGVTRHRWTGRYEAHLWDNSCKREGOTRKGROGGYDKEEKAARAYDL 2 350 AALKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQ 4
PRESTIT: 5  PRESTI	Db 286 AAIKFRGLNAVINLDMSRYDVESILSSDLPVGGGASGRAAAKFPLDSLQPGSAAANMLAG 345  Qy 477 ELARRKKDNDPRNKDI

Db 297 RAYDLAALKYMATATTNEPITNYSKEVEEMKHMTKQEFIASLRRKSSGFSRGASIYRGV 356  Qy 405 TRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAXDVAALKFRGANAVTNEPISRYDV 464	QIYDPRHHHN-QTGFYSDI  NWVAPTREFSTHQQVLEQQ ::DYLGHVVCVTAPSGI		R;Bevan, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X. submitted to the Protein Sequence Database, April 2000  A;Reference number: Z25026  A;Accession: T4998 A;Accession: T4998 A;Accession: T4998 A;Accession: DNA A;Residues: preliminary A;Residues: 1-566 < REV' A;Residues: 1-566 < REV' A;Residues: 1-566 < REV' A;Residues: 1-560 < REV' A;Residues: 1-560 < REV' A;Residues: 1-560 < REV' A;Residues: 1-560 < REV' A;Genetics: Cultivar Columbia; BAC clone F12B17 C;Genetics: A;Gene: ATSP:F12B17.140 A;Map position: 5 A;Introns: 33/1; 259/2; 287/1; 316/3; 341/2; 384/1 A;Residues: 33/1; 259/2; 287/1; 316/3; 341/2; 384/1 A;Gene: ATSP:F12B17.140 A;Map position: 5 A;Introns: 33/1; 259/2; 287/1; 316/3; 341/2; 384/1 A;Genery Match Colstination: 23.7%; Score 831; DB 2; Length 566; Best Local Similarity 36.1%; Pred. No. 8e-51; Matches 223; Conservative 69; Mismatches 167; Indels 158; Gaps 20;	Qy 537 ANGNGSDQKIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVT 596
RESULT 8  H96827  Protein F20B17.12 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: H96827 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.	115 YEEDIKEMESQSKEBYIGSLERKSSGFSRGVSKYRGVAKHHHNGRWEARIGRVFGNKYLY 428 LGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNLLAGELARRK    ::	141; Conservative 252 SQSSCVTAPSGTDS   : :	er, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; F Li, Y.; Lin, S.Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; N ey, T.; Rowley, D.; Sakano, H. berg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M. Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. ce and analysis of chromosome 1 of the plant Arabidops ber: A86141; MUID:21016719; PMID:11130712 6295 6295 6295 6295 6295 6296 6296 629	Qy 560 ALQDLIGIDSVGSGQHN 576  Db 534DSTGSNNNS 542  RESULT 7  D86295  Algories: Arabidopsis thaliana (mouse-ear cress) C. Species: Arabidopsis thaliana (mouse-ear cress) C. Pate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 C. Accession: D86295 R. Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Hulzar, L.

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RESULT 9
534116
534116
hypothetical protein - maize
c;Species: Zea mays (maize)
c;Species: Zea mays (maize)
c;Species: Zea mays (maize)
c;Ante: 08-Uul-1995 #sequence_revision 21-Uul-1995 #text_change 09-Sep-1997
c;Accession: S54116
R;Daniell, T.J.; Edwards, R.
submitted to the EMBL Data Library, January 1995
A;Beription: Complementation of a heat shock sensitive mutant of Escherichia coli defi
A;Reference number: S54116
A;Accession: S54116
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A;Accession: H96827
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-308 <STO>
A;Residues: 1-308 <STO>
A;Cross-references: GB:AE005173; NID:g7715603; PIDN:AAF68121.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-485 <DAN>
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Best Local S
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                  329
                                                                                                                                                                                                                                                            235 SVGC-GELQSLSLSMSPGSQSSCVTAPSGTDSVAVDAKKRGHAKLGQK-----QPVHR-- 286
                                                                                                                                                                                                                                                                                                                                                                 187 DCSSLMPQMTEGLKNWVAPTREFSTHQQVLEQQMNCG---MGNERNGVS-----LG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 HIWDNSCKKEGOTRKGROVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYOVOLE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 SSCVTAPSGTDSVAVDAKKRGHAKLGOKOPVHRKSIDTFGORTSOYRGVTRHRWTGRYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 17.6%; Score 616; DB 2 al Similarity 50.0%; Pred. No. 5e-36; 132; Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 SDKTASASESASIALTSKRK-----RKSPPRNAPL----QRSSPYRGVT--RWTGRYEA
                                                                                                                                                                                                            58 GVGCVGAPRSRRLQIR-----ITSLCAASCGSITARFLRHYPAAQSGTTVGEPLSRFT 110
                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
  GRQVYLGGYDKEEKAARAYDLAALKFWGPTTTTNFQVSNYEKELEEMKSMTRQEFIASLR
                                               GROVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLR 388
                                                                                                       LAAMSSTDVAWAESDQASGPPRRSASAHPSTVASPGTGGRGDMRRTCGNNSCRREGQSRK 170
                                                                                                                                                       ----KSIDTFGQRTSQYRGVTR-----HRWT-----GRYEAHLWDNSCKKEGQTRK 328
                                                                                                                                                                                                                                                                                                                 DMSSAYPH-----HWLSFSLSNNYHHGLLEAFSNSSGTPLGDEQGAVEESPRTVEDFLG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SREPESSODNK----SPKSEEVIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---NKDIDYNKSVVTSVNNEETVQ 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEEAAIAYDIAAIEYRGLNAVTNFDVSRY-----LNPNAAADKADSDSKPIRSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMEGQSKEEYIGSLRRKSSGFSRGVSKYRGVARHHINGRWEARIGRVFGNKYLYLGTYAT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFST 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIMDKNSWNDTQTKKGRQ---GAYDEEEAAARAYDLAALKYWGRDTLLNFPLPSYDEDVK 122
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          15.2%; Score 534; DB 2; Length 485; 33.5%; Pred. No. 6.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                 48; Mismatches 146; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: A85436
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                           APETALA2 protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Pate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C;Accession: A85436 C;Accession: A85436 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
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aintegumaenta-like protein - Arabidopsis thaliana
N.Alternate names: protein T12E18.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Jate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47591
R;Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Mewe submitted to the Protein Sequence Database, March 2000
A;Accession: T47591
A;Accession: T47591
A;Accession: T47591
A;Status: preliminary
A,Status: preliminary
A,Molecular recommendations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-205 <ELOS
A;Cross-references: EMBL;AL112971
A;Experimental source: cultivar Columbia;
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A; Introns: 71/2; 99/1; 128/3; 170/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: T12E18.10
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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180
                                                416
                                                                                                120 GPDTILNFPAETYTKELEEMQRVTKEEYLASLRRQSSGFSRGVSKYRGVARHHHNGRWEA 179
                                                                                                                                                                                                                                                          296 TSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYW 355
                                                                                                                                                                                                                                                                                                                                                                   241 LQSLSLSMSPGSQ-SSCVTAPSGTDSVAVDAKKRGHAK----LGQKQPVHRKSIDTFGQR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 GVMWGATSGAVVGQQDSSSKQGNGYASN 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRAQRRHQLDMSRYDVESILSSDLPVGGGASGRAAAKFPLDSLQPGSAAAMMLAGAAAAS
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                                             RIGRVAGNKDLYLGTFST 433
                                                                                                                                                   GPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQA
                                                                                                                                                                                                         SSIYRGVTRHRWTGRFEAHLWDKSSWNSIQNKKGKQ---GAYDSEEAAAHTYDLAALKYW
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                                                                                                                                                                                                                                                                                                             LTTSTCSSSPSSSVSSSTTTSSPIQSBAPRPKRAKRAKKSSPSGDKS--HNPTSPASTRR
                                                                                                                                                                                                                                                                                                                                                                                                                14.8%; Score 517; DB 2; ilarity 55.1%; Pred. No. 2.7e-29; Conservative 21; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAC clone T12E18
                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 205;
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                                                                                                                                                                                                                                                           R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, I. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C. Nature 402, 761-768, 1999

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of Chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; FMID:10617197

A;Accession: B84845
                                                                                                                                                                                                                                                                                                                                                                                                   probable AP2 domain transcription factor [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: B84845
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                                                                                                                      A; Gene: At2g41710
A; Map position: 2
                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-436 <STO>
A; Cross-references: GB:
                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                               ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 163; Conservative
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                                           Matches
                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 YQAPLEEETTKETH------VSDCSSLMPQMTEGLK----NWVAPTREFSTHQQVLE 217
  245 SLSMSPGSQSSCVTAPSGTDSVAVDAKK-----RGHAKLGQ------KQPVHRKSIDTFG 293
                                       137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 QQMNCGMGNERNGVSLGSVGCGELQSLSLSMSPGS-----QSSCVTAPSGTDSVAVD 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 MDSNGG-----GVASG------FPRAHWFGVKFCQSDLATGSSAGKATNVA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGMLNHTPNSNHQFPGSSNIGSGGGFSLFPAAENHRFDGRASTNQVLTNAAASSGFSPHH 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----HNQIFNSTSTPHQNWLQTNGFQPPLNRPS 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGPSLLFPMPPMETKIVNPIGTSVTSWLPSPTVQ---MRPS 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGSGQH-----NMLDESSKIGI--HFS-----NTSSLVTSLSSSREASPEK 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNWSRQEYVAHLRR 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQAGNINNENDSEWKMVLFNHPSQQQQANGNGSDQKIMNCGNYRNSAFSMALQDLIGIDS 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GANAVTNFDISRYDVERIMASSNLLAGELARRKKDNDPRNKDIDYNKSVVTSVNNEETVQ 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSTGFPRGSSKYRGVTL-HKCGRWEARMGQFLGKKYVYLGLFDTEVEAARAYDKAAIKCN 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFR 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDDYDDDLKQMTNLTKEEFVHVLRR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A----AVVEPAQPL-KKSRRGPRSRSSQYRGVTFYRRTGRWESHIWD--C-----G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HQTQREEESEEFCYSSPSKRVGSFSNSSSSAVVIEDGSDDDELNRVRPNNPLVTHQFFPE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKDAVINFDPSIYDEELNAESSG------NPTTPQDHNLD------
                                         Conservative
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                                                                                                                                                                                   GB:AE002093; NID:g2887500; PIDN:AAC02777.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.8%;
                                                           14.2%; Score 497.5; DB 29.7%; Pred. No. 2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---KHKSQDMRLRMNQQQQD-----SLHSNEVLGLGQ 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66; Mismatches 150; Indels 142;
                                     73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 517; DB 2;
Pred. No. 8.3e-29;
                                         Mismatches
                                                                            DB 2;
                                       168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 432;
                                                                            Length 436;
                                       83;
                                       Gaps
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393 TPFLPSGSSLTSEVRSHISIEPETSEVTKTETSCSTYSYLP 433
                                                                                                        615 FPMPPMETKIVNPIGTSVTSWLPSPTVQMRPSPAISLSHLP 655
                                                                                                                                                                                                      355 GAAALSIQK----------SMYPLTSILTAPLITNYNTLDPLADPIIW 392
                                                                                                                                                                                                                                                                                                          555 SAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREASPEKRGPSLL 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                495 NKSVVTSVNNEETVQVQAGNNNNENDSEWKWVLFNHPSQQQQANGNGSDQKIMNCGNYRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 SKASEDANVEDAGTELKT-LEHTSHATEPYKAPNLGVLCGTORKEKEISSPSSSSALSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             438 AEAYDVAAIKFRGANAVTNFDISRYDVERIMASS-NLLAGELARRKKDNDPRNKDI--DY 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 DASASRMPGPEYFSNIHYGAGDDRGTEGDFLGSFCLERKIDLTGYIKWWGANKNRQPESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 YWGPGTLINPPVTDYTRDĹEEMONLSREEYLASLRRKSSGFSRGIAKYRGL-----OSRW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 QRTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 YWGPSTHINFSIENYQVQLEEMXMWSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRW 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 KRSSIYRGVTRHRWTGRYEAHLWDKSTWNQNQNKKGKQVYLGAYDDEEAAARAYDLAALK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 SSDQGPKTEAGCSGGGGGSSETVAASDQMLLYRGFKKAKKERGCTAKERISKMPPCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                  SQSPAFKSLEEKVLKIQE-SCNNENDENANRNIIN----MEKNNGKAIEKPVVSHGVALG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QARIGRV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----AGNKDLYLGTFSTQ------EEA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 199

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: C84686 RESULT 13 C84686 probable AP2 domain transcription factor [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-464 <STO> C; Accession: C84686 A;Cross-references: GB:AE002093; NID:g4510402; PIDN:AAD21489.1; GSPDB:GN00139 Genetics: Gene: At2g28550

Query Match 13.9%; Score 486.5; DB 2; Best Local Similarity 35.1%; Pred. No. 1.3e-26; Matches 136; Conservative 55; Mismatches 120; 371 QLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGT 430 216 DMKQVQNLSKEEFVHILRRQSTGFSRGSSKYRGVTL-HKCGRWEARMGQFLGKKYIYLGL 166 WESHIWD--C----258 TAPSGTDSVAVDAKKRGHAKLGQKQPVH-----RKSIDTFGQRTSQYRGVTRHRWTGR 310 206 TREFSTHQQVLEQQMNCGMGNERNGVSLG-----SVGCGELQSLSLSMSPGSQSSCV 257 57 TRAFTLSFDILKVGSSSG-GDESPAASASVTKEFFPVSGDCGHLRDVE-----GSSSS-- 108 YEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQV 370 ---RNWIDLSFORIGDGETKLVTPVPTPAPVPAQVKKSRRGPRSRSSQYRGVTFYRRTGR 165 --GKQVYLGGFDTAHAAARAYDRAAIKFRGVDADINFTLGDYEE 215 Indels 77; Gaps 274

Length 464;

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APPTALA2-like protein Glossy15 - maize
C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: T03981
R;Moose, S.P.; Sisco, P.H.
Genes Dev. 10, 3018-3027, 1996
A;Title: Glossy15, an APETALA2-like gene from maize that regulates leaf epidermal (A;Fitle: Glossy15, an APETALA2-like gene from maize that regulates leaf epidermal (A;Fitle: Glossy15, an APETALA2-like gene from MID:8957002
A;Keterence number: Z15175; MUID:97115883; PMID:8957002
A;Kotestion: T03981
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Kotestion: T03981
A;Kotestion: T03981
A;Kotestion: 1-446 (MOO)
A;Cross-references: EMBL:U41466; NID:91732030; PIDN:AAC49567.1; PID:91732031
A;Experimental source: strain inbred W64A; leaf
C;Genetics:
A;Gene: Glossy15
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indeterminate spikelet 1 - maize (;Species: Zea mays (maize) c;pate: 19-Feb-1999 #sequence_re' (;Accession: TO1574 R;Chuck, G.; Meeley, R.B.; Hake, Genes Dev. 12, 1145-1154, 1998
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Best Local Similarity
Matches 119; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGSQSSCVT----APSGTDSVAVDAKKRCHAKLGQ-----KQPVHRKSIDTFGQRTSQY
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                                                                                                                                                                                                              ---AAPDAAPERR 374
                                                                                                                                                                                                                                                                                                                              ANGNGSDOKIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMGKKYVYLGLYDTETEAAQAYDKAAIKCYGKEAVTNFDAQSYD-----
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ilarity 31.9%;
Conservative 7
                                                            #sequence_revision
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; Pred. No. 2.2e-26;
74; Mismatches 114;
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                                                              19-Feb-1999 #text_change 29-Oct-1999
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A;Experimental source: strain C;Genetics:
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381 SWAWQAQGSPHVPLHHSAASSGFSTAAGANGGMPLPSHPPAQFP
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                                                                                                                                                                                                                 rigrvagnkdlylgtfstqeeaaeaydvaaikfrganavtnfdisrydverimassnila
                                                                                                                                                                                                                                                                            GPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQA
                                                                                                                                                                                                                                                                                                             SSOYRGVTFYRRTGRWESHIWD--C-----GKOVYLGGFDTAHAAARAYDRAAIKFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SSKIGTHFSNTSSLVTSLSSSREASPEKRGPSLLFP 616
                                                                                         QANGNGSDQKIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDE-----
                                                                                                                          DTETEAIDDGDAIDLDLRISQPNVQDPKRDNTL---AGLQPTCDSPESSNTMASQPMSSS
                                                                                                                                                       GELARRKKOND PRNKD I DYNKS VVTSVNNEET VQVQAGNNNNENDSEWKMVL FNHPSQQQ
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ce: strain B73
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                                                                GYHONPAVSFHHORLYSSACHGFFPNHQVQERPVERRPELGAQPFP
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Pred. No. 2.6e-25;
B; Mismatches 164
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Search completed: March 9, 2004, 10:47:35
Job time: 23 secs

Scoring

table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of

hits satisfying chosen parameters:

141681 segs, 52070155 residues

DB 80

seq geq

length: length:

2000000000

Post-processing: Minimum Match

Maximum Match Listing first

100% 45 sı 80

summaries

SwissProt\_42:\*

Title: Perfect score:

US-10-024-632-2 3502 1 MKRINESNNTDDGN

Run on:

protein

1

protein search, using sw model

Copyright

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d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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P25391
P470391
P470399
Q9y6q9
P461339
P461367
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Q7yqm4
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RESULT 1

ARACHM STANDARD; PRT; 432 AA.

AC 275271996 (Rel. 33, Created)

PT 107521996 (Rel. 34, Last sequence update)

PT 107521996 (Rel. 33, Last sequence update)

PT 107521996 (Rel. 34, Last sequence update)

PT 107521998 (Rel. 34, Last sequence update)

  RA Mayer K.F.X., Schweller C., Wambutt R., Murphy G., Volckaert G., RA Mayer K.F.X., Schweller C., Wambutt R., Mirphy G., Volckaert G., RA Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Mueller M., Metches gartner M., de Simone V., Obermaier B., Mache R., Mueller M., Ra Reichert B., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Ra Reichert B., Wosheel J., Zimmermann W., Wedler H., Ridley P., Ra Reichert B., McCullagh B., Bilham L., Robben J., Vandenbussche F., Ra Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., Ra Vos P., Hoheisel J., Grymonprez B., Chuang Y.-J., Vandenbussche F., Ra Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F., Ra Meitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Rayer B., Van Staveren M., Dikse W., Ra Modjman P., Klein Lankborst R., Rose M., Hauf J., Koetter P., Ra Modjman P., Klein Lankborst R., Rose M., Hauf J., Koetter P., Ra Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., Ra De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R., Ra Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., Ra Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., Ra Clark L., Rajandream M.A., Lyne M., Benes V., Rechmann S., Rayiriou A., Vitale D., Liguori R., Piravandi E., Ra Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R., Ra Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., Ra Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., Ra Gibbons T., Weber N., Vandenbol M., Bargues M., Tacon D., Jesse T., Ra Perez Perez A., Purnelle B., Bent E., Johnson S., Tacos D., Jesse T., Ra Perez Perez A., Berger C., Monfort A., Casacuberta E., Bielke C., Field R., Eleke C., Field R., Berger C., Monfort A., Stocker S., Bielke C., Field R., Berger C., Monson S., Tacos D., Jesse T., Ra Perez Perez A., Berger C., Monson S., Stocker S., Bielke C., Field R., Berger C., Monson
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MIX1 CARELL
SPL1 COTUA
SPL1 COTUA
BPEB HUMAN
CYL1 BOVIN
PSU1 YEAST
TF20 MOUSE
FTSK YERPE
YMA6 YEAST
BUD4 YEAST
BUD4 YEAST
BUD4 YEAST
BUD4 YEAST
BUD4 YEAST
KINH LOLFEE
SBCC_PSEAE
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Result No.

Query Match

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SUMMARIES

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RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hamed A., Lodhi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.,
"Sequence and analysis of chromosome 4 of the plant Arabidopsis
IT thaliana.";
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[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sisb-sib.ch).
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Drews G.N., Bowman J.L., Meyerowitz E.M.;
"Negative regulation of the Arabidopsis h
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
EMBL;
PIR; A
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Cell 65:991-1002(1991).
                                                                                                                                                                                                                   PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_ERF; 1.
SMART; SMC0380; AP2; 2.
                                                                                                                                                                                                                                                                                                                 PIR; A85436; A85436.
TRANSFAC; TO1774; --
InterPro: IPR001471; TF ERF.
Pfam; PF00847; AP2-domain; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U12546; AAC13770.1; -. EMBL; Z99707; CAB16765.1; -. EMBL; AL161590; CAB80358.1;
                    DNIB_AND
                                                       DOMAIN
                                                                                                                                                                                    Flowering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUNCTION: Probable transcriptional activator that promotes early floral meristem identity. Is required subsequently for the transition of an inflorescence meristem into a floral meristem. Plays a central role in the specification of floral identity, particulary for the normal development of sepals and petals in the wild-type flower. Acts as A class cadastral protein by repressing the C class floral homeotic gene AGAMOUS in association with others repressors like LEUNIG and SEUSS. It is also required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homeotic protein AGAMOUS in stamens and carpels.
MISCELLANBOUS: Mutations in the APETALA2 gene result in the actopic expression of AGAMOUS, leading to the replacement sepals by carpels and stamens and of petals by stamens.
SIMILARITY: Contains 2 AP2/ERF domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  shoot apex, and at enhanced levels in the inflorescence meristem, young floral buds, and throughout the early stages of flower development and organogenesis. During floral organ differentiation it becomes spatially restricted to specific organ, tissue, and cell types within the flower.

INDUCTION: Negatively regulated by the C class floral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: Sepals, petals, stamens, carpels, developing ovules, inflorescence stem, leaf, and stem.

DEVELOPMENTAL STAGE: It is detectable at low levels throughout
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  during seed development.
SUBUNIT: May form homodimer.
SUBCELLULAR LOCATION: Nuclear (Probable).
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OSBO; AFZ, ...

Transcription regulation; Activator; Development Front Process of the Control of
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Shah R.,
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Pathogenesis-related ge
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
lamiids; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKUMSRQEYVAHLRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKKRGHAKLGQKQPVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRKG
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G->E: TEMPERATURE S
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eudicots; asterids;
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AP2-5.
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Zhou J., Tang X., Martin G.B.;
"The Pto kinase conferring resistance to tomato bacterial disease interacts with proteins that bind a cis-element of

speck

SEQUENCE FROM N.A. MEDLINE=97357308; PubMed=9214637;

pathogenesis-related genes."; EMBO J. 16:3207-3218(1997).

J. 16:3207-3218(1997).
FUNCTION: Transcription
pathogenesis-related pro

genes. SUBUNIT:

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promoter

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  REPRESENTATION OF THE PROPERTY OF THE PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSSXB3; Q9NHN1; Q9NJ17; Q9U6C3; Q9VPL1; Q9VPL2; 10-QCT-2003 (Rel. 42, Created) 10-CCT-2003 (Rel. 42, Last sequence update) 10-CCT-2003 (Rel. 42, Last annotation update) Spilt ends protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Contains 1 AP2/ERF domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00380; AP2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFAC; TU4/1/; TF ERF.
InterPro; IPR001471; TF ERF.
Pfam; PF00847; APZ-domain; 1.
PRINTS; PR00367; ETHRSPELEMNT.
PRODOM; PD001423; TF ERF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; O80337; 2GCC.
TRANSFAC; T04717;
                                                                                                                                                                                                                                    Wiellette E.L., McGinnis W.;
MEDLINE=20157049; PubMed=10655223; Rebay I., Chen F., Hsiao F., Kolod Suh C., Voas M., Williams A., Rubi
                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                                                        USAGE,
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                       MEDLINE=20025936;
                                                                                                                                                                                                                                                                                                                TISSUE=Embryo;
                                                                                                                                                                        repress the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; U89257; AAC49741.1; -. T07728; T07728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ends protein.
OR CG18497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
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                                                                                                                                                                                                                                                                                                                                                           TISSUE
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                                                                                               FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVAGNKDLYLGTFSTQEBAABAYDVAAIKFRGANAVTNFDISRYDVERIMASSNLLAGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEINLMPSTKSIGDRKRRSVSPDSDVT--RRKK-----FRGV-RORPWGRWAAEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THINESIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARRKKONDPRNKDIDYNKSVVTSVNNEETVQVQAGNNNNEND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPTRGKRVWLGTYDTPEEAAVVYDKAAVKLKGPDAVTNFFVST---
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ilarity 29.0%;
Conservative 1
                                                                                                                                               126:5373-5385(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulation; DNA-binding; Activator; Nuclear 95 AP2/ERF.
                                                                                               N.A.
                                                                                                                                                                                       an RNP motif
e development
                                                                                                                                                                                                                                                                                                                                                        N.A. (ISOFORMS 3 AND 4), FUNCTION, SPECIFICITY, DEVELOPMENTAL STAGE,
  F., Hsiao F., Kolodziej P.A.,
., Williams A., Rubin G.M.;
                                                                                                                                                                                                                                                              Harding
                                                                                                                                                                                                                                                              PubMed=10556062;
arding K.W., Mace
                                                                                                  (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27913 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -TAEVTVTVTETETESVADGGDKSEND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                %; Score 156.5;
%; Pred. No. 0.0
16; Mismatches
                                                                                                                                                                                            protein that of head-like
                                                                                                  4.
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                                                                                                                                                                                                                                                                K.A.,
                                                                                                                                                                                               interacts
sclerites
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                           Kuang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ecta; Pterygota; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
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                                Laverty
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SEQUENCE OF 424-2002 FROM N.A. STRAIN=Berkeley; TISSUE=Embryo; MEDLINE=22426066; PubMed=125375

systematic r Genome Biol.

review

3:RESEARCH0083.1-RESEARCH0083.22(2002)

Lewis S.E.

"Annotation of the Drosophila melanogaster

euchromatic

genome:

1 K.S., k S.E., an B.P.,

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Handan R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxrer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Markin, D., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Blasm D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Ghorya D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier S.M.,
RA Ghodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Golden K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Matuch F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA McMand B.E., Kodira C.D., Kraft C., Kravitz S., Kulj D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulj D., Lai Z.,
RA McMallov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Naxon K., Nusskern D.R., Nelson D.L.,
RA Manderson D.R., Nelson K.A., Sanders R.D.C., Scheeler F., Shen H.,
RA Martin J., Maller J., Louders R., Pealeb J.M.,
RA Martin J., Waller J., Louders R., Pealeb J.M.,
RA Martin J., Maller J., Landers R., Deng R., Sun E.,
RA Martin J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein kinase signaling pathway that interact with the yan gene of Drosophila identifies split ends, a new RNA recognition motifiented and interact signaling pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20171275; PubMed=10704397; Kuang B.H., Wu S.C.-Y., Shin Y.-A., Luo L., Kolodziej P.A.; Kuang B.H., Wu S.C.-Y., Shin Y.-A., Luo L., Kolodziej P.A.; "split ends encodes large nuclear proteins that regulate neuronal cell fate and axon extension in the Drosophila embryo."; pevelopment 127:1517-1529(2000).
                                                                                                                                                                     REVISIONS, AND ALTERNATIVE SPLICING.

MEDLINE=22426069, PUNMed=12537572,

Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.

smith C.D., Tupy J.L., Whitfield E.J., Bayrakkarogiu L., Berman B.

Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Embryo;
MEDLINE=20171275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISOFORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND
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Lane M.E., Lehner C.F.
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"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH080.1-RESEARCH088.8 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A screen for modifiers of cyclin E functi
melanogaster identifies Cdk2 mutations, re
of putative phosphorylation sites in Cdk2.
Genetics 155:233-244(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "split ends, a new component of the regulates development of midline gli Curr. Biol. 10:943-946(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen F., Reb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20253107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22668876; PubMed=12783785;
Lin H.V., Doroquez D.B., Cho S., Chen F., F
"Splits ends is a tissue/promoter specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stapleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signaling.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20414403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION ON
                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION ON WG PATHWAY
                                                                                                                                                                                               Name=4; Synonyms=SpenS;
IsoId=Q85X83-4; Sequence=VSP 008565, VSP 008567;
Note=Produced by alternative splicing of isoform 2;
Note=Springing the production of isoform 2;
In stage 3 embryos, and in blastoderm cells, including pole cells.
Expressed throughout the rest of embryogenesis. Later, it is expressed at higher level in epidermal cells and CNS.
DEVELOPMENTAL STAGE: Isoform 3 is expressed both maternally and
                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins.
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
Event=Alternative promoter;
Comment=2 isoforms, 1 (shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Probable corepressor protein, which regulates different key pathways such as the EGF receptor and Wg pathways. Involved in neuronal cell fate, survival and axon guidance, cell cycle regulation and repression of head identity in the embryonic trunk. May act with the Hox gene Deformed and the EGF receptor signaling pathway. Positive regulator of the Wg pathway in larval tissues but not in embryonic tissues. May act as a transcriptional corepressor protein, which repress transcription via the recruitment of large complexes containing histone deacetylase
                                                                                                          zygotically.

SIMILARITY: Belongs to the Spen family.

SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.

SIMILARITY: Contains 1 SPOC domain.

CAUTION: It is uncertain whether Met-1 or Met-7 is the initiator.
                                                                                                                                                                                                                                                                                                                       Name=2;
IsOId=Q88X83-2; Sequence=VSP 008565, VSP 008566;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lopment 130:3125-3135(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q8SX83-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kebay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR PATHWAY.
3; PubMed=10959845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=10790398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  splicing; Named
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W., Brokstein P., Yu C., Ch. Kronmiller B., Pacleb J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (shown here)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Drosophila
glial cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     isoforms=4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marzodko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which regulates different
nd Wg pathways. Involved in
                                                                                                                                                                                                                                                                                                                               of isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in Drosophila
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PROSITE; PS00030; RRM_RNP_1; FALSE_NEG-PROSITE; PS50917; SPOC; 1.
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Pfam; PF00076; rrm; 3.
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Local Similarity
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                                         QQQQANGNGSDQKIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGT-----
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AAF26299.1;
AAF234661.1;
AAF51534.2;
AAF51535.2;
AAN10511.1;
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X Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

A Yamada K., Lim J., Dale J.M., Chen H., Pham P.K., Cheuk R.F.,

A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

A Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

A Miranda M., Quach H.L., Tripp M., Chang J.M., Akiyama K., Ansari Y.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

A Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

A Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

A Kaniya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

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A Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
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Brover V., Troukhan M., Alexandrov N., Lu Y.-P. Feldmann K.A.; Feldmann K.A.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ of the EMBL/GenBank/DD
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proteins in Arabidopsis.";
proteins in Arabidopsis.";
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Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty P1 and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=97338147; PubMed=9192694;
Okamuro J.K., Caster B., Villarroel R., van Montagu M., Jofuku K.D.;
"The AP2 domain of APETALA2 defines a large new family of DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baek E., Lee S.; (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Columbia;
                                                                                                                                                                                                       Troukhan M., Alexandrov N., Lu Y.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Columbia;
                                                                                                                                                                                                          Flavell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rosids;
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RRR OOCOON BITTO

SEQUENCE FROM N.A.
TISSUE=Seedling;
MEDLINE=99081843; PubMed=9862967;

NCBI\_TaxID=3702;

core eudicots; rosids;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z37504; CAA85734.1; ALT_SEQ.
EMBL; AF003096; AAC49769.1; --
EMBL; AP003097; BAB02769.1; --
EMBL; AY059917; AAL24999.1; --
EMBL; AY05910; AAK29605.1; --
EMBL; AY042562; AAN13131.1; --
EMBL; AY057488; AAN65031.1; --
EMBL; AY067488; AAN65031.1; --
EMBL; AY0674888; AX0674888; AX06748888; AX067488888; AX0674888888; AX067488888; AX067488888; AX067488888; AX067488888; AX067488888; AX06748888; 
                             JT 5
ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
RAV1_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; DNA-binding; Nuclear protein; Cadmium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00380; AP2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_ERF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001471; TF ERF.
Pfam; PF00847; AP2-domain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RANSFAC; T02658;
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                                                                                                                                                                 205 KQQISSLESFLELDGNTAEQPSQLDES
                                                                                                                                                                                                                                   555 SAFSMALQDLIGIDSVGSGQHNMLDES 581
                                                                                                                                                                                                                                                                                                    164 CVV------SQSESE-----LSQPSFPVECIGFGNGDEFQNLSYGFEPDYDL
                                                                                                                                                                                                                                                                                                                                                                      500 TSVNNEETVQVQAGNNNNENDSEWKMVLFNHPSQQQQANGNGSDQKIMNCG-----NYRN
                                                                                                                                                                                                                                                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 AYDVAAIKFRGANAVTNFDISRYDVERIMASSNLLAGELARRKKDNDPRNKDIDYNKSVV 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 RQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAE 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 KGRQVYLGGYDMEEKAARAYDLAALKYWG-----PSTHINFSIENYQVQLEEMKNMS 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 ATEPGKRRKKK-----NVYRGI-RKRPWGKWAAEIRDPRKGVRVWLGTFNTAEEAAM 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 KGRKL----TAEELWSELDASAADDFWGFYSTSKLHPTNQVN-----VKEEAVKKEQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            AYDVAAKQIRGDKAKLNFPDLHHP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TF_ERF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27758 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 147;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP2/ERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317D50CC514782F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            --PPPNYTPPPSSPRSTDQPPAKK
344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.0033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100;
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MEDLINE-21016719; PubMed=11130712;

With Edition of the planm C.L., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler B., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A. Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan A., Lam B.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan A., Lam B.,

A. Hinter J.L., Jenkins J., Johnson-Hopson C., Khan A., Lam B.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan A., Lam B.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan A., Lam B.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan A., Lam B.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan A., Lam B.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan B.,

Hunter J.L., Was J., Liu Z., Li
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"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22954850; PubMed=14593172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "RAVI, a novel DNA-binding protein, binds to bipartite recognition sequence through two distinct DNA-binding domains uniquely found in higher plants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression in flowers.

DOMAIN: Contains two distinct DNA-binding domains. One is located in the N-terminal region and binds to the 5'-CAACA-3' motif. The second is located in the C-terminal region and binds to the 5'-CACCTG-3' motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ence 302:842-846(2003).

FUNCTION: Binds specifically to bipartite recognition sequences composed of two unrelated motifs, 5'-CAACA-3' and 5'-CACCIG-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 1 AP2/ERF domain.
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TISSUS SPRCIFICTY: Expressed in all tissues examined: Roots,
rosette leaves, cauline leaves, inflorescence stems, flowers ar
siliques. Highest expression in roots and rosette leaves. Very
                                                 AB013886;
AC011810;
AY063855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408:816-820(2000).
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; BAA34250.1; -.; AAG09554.1; -.; AAL36211.1; -.; AAM14230.1; -.
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Best Local &
STRAIN=ev. Columbia;

STRAIN=ev. Columbia;

STRAIN=ev. Columbia;

MEDLINE-21016720; PhiMed=11130713;

Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

Salanoubat M., Lemcke K., Rieger M., Perez-Alonso M., Obermaier B.,

Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier P.,

Delseny M., Boutry M., Grivell L.A., Mache F., Robert C., Brottier P.,

De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,

Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

Wincker P., Cattolico L., Weissenbach J., Saurin W., Ouetier F.,

Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,

Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,

Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura

Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura

Wiedelman, K., Kranz H., Pallavicini A., Toppo S., Simionati B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; T51329; T51329.
HSSP; O80337; ZGCC.
InterPro; IPR003340; TF_B3.
InterPro; IPR001471; TF_RRP.
Pfam; PF00847; APZ-domain; 1.
Pfam; PF02362; B3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ethylene responsive element binding factor 4 (Aterf4).
ERF4 OR ERF-4 OR AT3G15210 OR K7L4.1.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots; rosidencesids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujimoto S.Y., Ohta M., Usui A., Shinshi H., Ohme-Takagi M., "Arabidopsis ethylene responsive element binding factors act transcriptional activators or repressors of GCC box mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_ERF; 1.
DNA-binding; Nuclear_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ant Cell 12:393-404(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   544 QKIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              484 DNDPRNKDIDYNKSVVTSVNNEETVQVQAGNNNNENDSEWKMVLFNHPSQQQQANGNGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 SROEYVAHLRRKSSGFS-------RGASIYRGVTRHHQHGRWQARIGRVAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424 KDLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNLLAGELARRKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25
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38597 MW;
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23.4%; Pred. No. 0.013;
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RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vicale D.,
RA Mayer K.F. X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Mayer K.F. X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
Wa Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
Wa Salamoto A., Yasuda M., Tabata S.;
"Sequence and analysis of chromosome 3 of the plant Arabidopsis
"T thaliana.","
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 67
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InterPro; IPR001471; TF_ERF.
Pfam; PP00847; AP2-domain; 1.
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_ERF; 1.
SMART; SM00380; AP2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB008106; BAA32421.1; -. EMBL; AP000413; BAB02150.1; -.
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; O80337; 2GCC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    458 --DISRYDVERIMASSNLLAGELARRKKUNDPRNKDIDYNKSVVTSVNNEETVQVQAGNN 515
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                                                                 --PPME 621
                                                                                                                                                                                                                                                                                        GNV-
                                                                                                                                                                                                                                                                                                                                                      NNENDSEWKMYLFNHPSQQQQANGNGSDQKIMNCGNYRNSAFSMALQ-----DLIGIDS 569
                                                                                                                                                                                                                                                                                                                                                                                                                           YRGV-RKRPWGRYAAEI-RDPGKKTRVWLGTFDTAEEAARAYDTAARDFRGAKAKTNFPT 82
                                                                                                                                                                                                               VGSGQHNMLDESSK------IGTHFSNTSSLVTSLSSSREASPEKRGPSLLFPM- 617
                                                                                                                                          VGRGQPPPVTSAFRSPVVHVATKMACGAQSDSDSSSVVDF----EGGMEXRSQLLDLDLN 214
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J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on regulation; DNA-binding; Nuclear protein.
22 86 AP2/ERF.
132 137 POLY-GLY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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RESULT 7

ERF2_APAT

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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ethylene responsive element binding factor 2 (Atere).
ERR2 OR ERF-2 OR AT5647220 OR MQL5.7.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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080338;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20181733; PubMed=10715325; MEDLINE=20181733; PubMed=10715325; Fujimoto S.Y., Ohta M., Usui A., Shinshi H., Ohme-Takagi M.; "Arabidopsis ethylene responsive element binding factors act transcriptional activators or repressors of GCC box mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_ERF; 1.
SMART; SM00380; AP2; 1.
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EMBL; AB018117; BAA97155.1; ~.
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Pfam; PF00847; AP2-domain; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC; T04634; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structural analysis of Arabidopsis thaliana chromosome 5. X. Se features of the regions of 3,076,755 bp covered by sixty Pl and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Transcription factor that binds to pathogenesis-related promoter element. SUBCELLULAR LOCATION: Nuclear (Probable). SIMILARITY: Contains 1 AP2/ERF domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T51989; T51989.
                                                                                                                                                                  302 VTRHRWTGRYEAHLWDN-----SCKKEGQTRKGRQVYLGGYDMEEKAAR---AYDLA--A
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                                                     352 LKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHG
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68 FHFDTSSSDLSCLFDFPAVKVEPTENFTAMEEKPKKAIPVTETAVKAKHYRGV-RORPWG
                                                                                                                                                                                                                                                             Similarity
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                                                                                                             ITRHULGGGGENELRLNESTPSSCFTES--
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                                                                                                                                                                                                                                                                                                                                           243 AA;
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  regulation; DNA-binding; Nuclear 23 26 POLY-GLY.
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Pred. No. 0.026;
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; C9A4C9791249B5D4 CRC64;
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16-OCT-2001 (Rel. .
15-MAR-2004 (Rel. .
Cyclin T1 (Cyclin .
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STRAIN=(57BL/6; TISSUE=Brain;
MEDLINE=99651315; PubMed=9832504;
MEDLINE=99651315; PubMed=9832504;
Garber M.E., Wei P., KewalRamani V.N., Mayall
Rice A.P., Littman D.R., Jones K.A.;
The interaction between HIV-1 Tat and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99059742; PubMed=9843510;
Blenlasz P.D., Grdina T.A., Bogerd H.P., Cullen B
"Recruitment of a protein complex containing Tat
governs the species specificity of HIV-1 Tat.";
EMBO J. 17:7056-7065(1998).
                                                                                                                                                                                  MEDINE=99145542; PubMed=9990016;
Fujinaga K., Taube R., Wimmer J., Cujec T.P., Peterlin B.M.;
Fujinaga K., Taube R., Wimmer J., Cujec T.P., Peterlin B.M.;
Interactions between human cyclin T, Tat, and the transactivation
response element (TAR) are disrupted by a cysteine to tyrosine
substitution found in mouse cyclin T.";
Proc. Natl. Acad. Sci. U.S.A. 96:1285-1190(1999).
Proc. Natl. Acad. Sci. U.S.A. 96:1285-1290(1999).
Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99263519; PubMed=10329126; Kwak Y.T., Ivanov D., Guo J., Nee "Role of the human and murine cycl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and a critical cysteine residue that is CycTl protein.";
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"Role of the human and
                                                                                  SUBUNIT: Associates with CDK9 to form P-TEPEB predominant cyclin associated with CDK9 (By B: SUBCELLULAR IOCATION: Nuclear (By similarity) SIMILARITY: BELONGS TO THE CYCLIN FAMILY. STR
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SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the En
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                                                                                                                                              ---KPEEIKMRIKVHSAGDKHNSIEDSVTKSREHKEKORTHPSNHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                          -----DHSLQQDGSSAFGSQKQASKSVPSAKVSLKEY----RAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -ILNMISQTSSDTT-----
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Pfam; PFUULDS; CYCLIN; 1.
SMART; SM00385; CYCLIN; 1.
PROSSITE; PS00292; CYCLINS; FALSE NE
CYClin; Cell cycle; Cell division;
Cyclin; Cell cycle; Cell division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF095640; AAD13656.1; --
EMBL; AF109179; AAD19654.1; --
EMBL; AF087662; AAD17798.1; --
EMBL; AF113951; AAD17205.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006670; Cyclin.
InterPro; IPR006671; Cyclin_N.
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                                                                                                                                                                                                                                                                                                                      FALSE NEG
                                                              POLY-SER.
COILED COIL (POTENTI
POLY-HIS.
POLY-SER.
POLY-PRO.
V -> M (IN REF. 3).
W; 7396E428F5A8B91B C
Score 134;
Pred. No. 0
                                                                                                                                                                                                                      lear protein.
NUCLEAR LOCALIZATION SIGNAL
NUCLEAR COCALIZATION MOTIF (T
                                                                                                                                                                                                                                                                                              Coiled
  . 12 j
                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                              coil;
                     1:
                        Length
                                                                     CRC64;
                                                                                                                                                                                                                               (TRM)
                                                                                                                                                                                                                                                     (POTENTIAL).
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LGFELTIDHPHTHVVKCTQLVRASKDLAQTSYFMATNSLHLTTFSLQY -PH-----MKMEATSAATVPTTFYMSPSQSHLSNFGMCYGVGENGNFHSPL 96; Mismatches 197; Indels 278; -----TPP THEYGSHERG Gaps 122 69 194

ANGNGSDOKIMNCGNYRNSAFSMALQDLIGIDSVG

571 520 519 474

545

--NPERPFLDKADKSALKMRLPVASGDKAVSS---

QLENMEANVKSQY-----

----AYAAQNL

425

404 395 344 353

459

-VYLGGYDMEEKAA

----ADENTSEQ

281

182 241

242

-----IA

297

69

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RX MEDLINE=9930751; PubMed=10373508;
RX MEDLINE=9930751; PubMed=10373508;
RX MEDLINE=9930751; PubMed=10373508;
RX MEDLINE=9930751; PubMed=10373508;
RT Highly divergent lentiviral Tat proteins activate viral gene
RT "Highly divergent lentiviral Tat proteins
RT expression by a common mechanism.";
RM Mol. Cell. Biol. 19:4592-4599(1999).

CC (CDM9/cyclin T) complex, also called positive transcription
CC (CDM9/cyclin T) complex transcriptional activator, Tat. It is
CC (CDM9/cyclin associated with CDM9 to form -TEPB. Cyclin T] is the
CC (CDM9/cyclin associated with CDM9 (By similarity).
CC (COMPONITY: Belongs to the cyclin family. Cyclin C subfamily.
CC (COMPONITY: Belongs to the cyclin family. Cyclin C subfamily.
CC (COMPONITY: Belongs to the cyclin family. Cyclin C subfamily.
CC (COMPONITY: Belongs to the cyclin family.
Cyclin C subfamily.
CC (COMPONITY: Belongs to the cyclin family.
Cyclin C subfamily.
CC (COMPONITY: Belongs to the cyclin family.
Cyclin C subfamily.
Cyclin C subfamily
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Query Match
Best Local Sim
Matches 137;
                                                                                                                                                  DOMAIN
                                                                                                                                                                                                            SMART; SM00385; CYCLIN; 1.

PROSTIE; P800292; CYCLINS; FALSE NEG.

Cyclin; Cell cycle; Cell division; Coiled coil;

Transcription regulation; Nuclear protein.

DOMAIN 253 270 VUCLEAR LOCALIZATION SIGNAL DOMAIN 254 272 TAT:TAR RECOGNITION MOTIF (T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCT1 F
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006670; Cyclin.
InterPro; IPR006671; Cyclin_N.
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF137509; AAD38518.1; -.
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                                                                                                                                                                                                                                                                                                                       Pfam; PF00134; cyclin; 1
SMART; SM00385; CYCLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata
Mammalia; Eutheria; Perissodactyla; Equidae; Equus
                                                                                     SEQUENCE
                                                                                                             DOMAIN
                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
Cyclin T1 (Cyclin T) (CycT1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HORSE
                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SLLFPMPPMETKIVNPIGTSVTSWLP--SPTVQMR 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----HSSQTSTLAHKTYSLSSTLSSS--SSTRKRGPPEETGAAVFDHPAKIAKSTK 595
    Conservative
                                                                                     $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                       3.7%;
                                                                                     81013 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
s; Score 129.5; D
s; Pred. No. 0.26;
80; Mismatches
                                                                                                                             SIMILARITY).
COILED COIL (POTENTIAL)
POLY-HIS.
POLY-SER.
                                                                                                             POLY-PRO
                                                                                        BFC2A398D6B35BCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  727 AA.
                                            DB 1;
    221;
    Indels 243;
                                         Length
                                                                                                                                                                                                                     (TRM)
                                                                                                                                                                                                                                     (POTENTIAL).
Gaps
  31;
    RRRRRRR OCCOGGETA
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080341; Q91VT6;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ethylene responsive element binding factor 5 (AtERF5).
ERF5 OR ERF-5 OR ATSG47230 OR MQL5_9.
                  expression.";
Plant Cell 12:393-404(2000)
                                                                                   Fujimoto S.Y., Ohta M., Usui A., Shinshi
"Arabidopsis ethylene responsive element
                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid.

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARATH
                                                                 transcriptional activators or repressors
                                                                                                                           MEDLINE=20181733; PubMed=10715325;
                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    635 WLPSPTVQMRPSPAISLSHLP 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 HGRWQARIGRVAGNKDLYL-----GTFSTQEEAAEAYDVAAIKFR-----GANAVTNFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 -YRGVTRHRWTGRYEAHLWDNSCKKEG------QTRKGRQVYLGGYDMEE-KAARAYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 LGFELTIDHPHTHVVKCTQLVRASKDLAQTSYFMATNSLHLTTFSLQY------TPP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 VV-----ACVCIHLACKWSNWEIPVSTDGKHWWEYV-DATVTLELLDELTHEF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPPLPTMAQLPGHSSDTSGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESSKIGTHESNISSLVISLSSSREASPEKRGP----SLLEPMPPMETKIVNPIGISVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AALKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOSLSLSMSPGSQSSCVTAPSGTDSVAVDAKKRGHAKLGQKQPVHRKSIDTFGQRTSQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSLDSIYYNSQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETTKE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSEWKMVLFNHPSQQQQANGNGSDQKIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----AŚŚK--PEEIKMRIKVHAAPDKHNSIDDSVTKSREHKEKHKTHPSNHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRYDVERIMASSNILLAGELARRKKDNDPRNKDIDYNKSVVTSVNNEETVQVQAGNNNNEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKADD~-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYMPLKSDGSLCILEALKRSQTQVMVPTSSPKLEDFLGGATMG-----THEYGSHERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGFSLS---PH-----MKMEATSAATVPTTFYMSPSQSHLSNFGMCYGVGENGNFHSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -SSQTSTLAHKTYSLSSSFSSS--SSSRKRGPPEETGGALFDHPAKIAKSTK--SSSINF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SHSSVILKMPIEGSENPERPFLEKPDKTALKMRIPVASGDKA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LMSMSTSSTTSTVPSLPTTEESSSNLSGVEMLQGERWLSSQPPF---KLEPAQGHRTSENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLEQQMNCGMGNERNGVSLGS--VGCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --NHHSHK-----HSHSQLPAGTGNKR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LOILEKT PURLKRIRUWR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------AYAAQNLLSHHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----RGTDENTSEQTIL-----NMISQSSSDTTIAG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---DHSLQQDGSNAFISQKQNSSKSVPSAKVSLKEYRAKHAEEL
                                                              H., Ohme-Takagi M.;
binding factors act
of GCC box mediated
                                                                                                                                                                                                                                        core eudicots; rosids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QAAKK 266
                                                                 gene
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474 459 432 409 402

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RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Lkiyama K., Ansari Y.,
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Arakawa T., Dahnson-Hopson C., Hsuan V.M., Jida K., Karnes M.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.M., Jida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Sakurai T.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Sakurai T.,
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
Tempirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                           Query Match
Best Local (
                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                        HSSP; O80337, 2GCC.
TRANSPAC; T04637;
InterPro; IPR001477; TF ERF.
InterPro; IPR001477; APZ-domaIn; 1.
Pfam; PF00847; APZ-domaIn; 1.
PRINTS; PR00367; ETHRSPELEMNT.
PRODOM; PD001423; TF ERF; 1.
SMART; SM00380; APZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB008107; BAA32422.1; -.
EMBL; AB018117; BAA97157.1; ALT INIT.
EMBL; AF385709; AAK63301.1; -.
EMBL; AY078014; AALT7715.1; -.
EMBL; AX17568; BAC42229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Ki Hayashizaki Y., Shinozaki K., "Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: Transcription factor that binds to the GCC-box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structural analysis of Arabidopsis thaliana chromosome 5. ) features of the regions of 3,076,755 bp covered by sixty Pl clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as rong to sage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                Transcription regulation; DNA-binding; Nuclear protein.
DOMAIN 51 55 POLY-SER.
DNA_BIND 153 218 AP2/ERF.
                                                                                                                                                                                                                                                                                   DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; T52020; T52020.
HSSP; O80337; 2GCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22954850; PubMed=14593172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathogenesis-related promoter element.
SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: Contains 1 AP2/ERF domain.
349 LAALKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRXSSGFSRGASIYRGVTRHH 408
                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20181125; PubMed=10718197; Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                                                    300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Columbia;
                                                                                                            Conservative
                                                                                                                                                                                                                                                        33810 MW;
                                                                                                                                           3.7%;
                                                                                                        %; Score 128.5; DB
%; Pred. No. 0.084;
24; Mismatches
                                                                                                                                                                                                                                                        1189D464A28F7251 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Akiyama K., Ishida J.,
ka M., Carninci P., Kawai J.,
                                                                                                                                                                          DB 1;
                                                                                                            66;
                                                                                                                                                                              Length
                                                                                                            Indels
                                                                                                                                                                                  300;
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1 and TAC
                                                                                                            49;
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RAD9
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                                                                                                                                                                                                                                                                        vialard J.E., Gilbert C.S., Green C.M., Lowndes N.F.;
"The budding yeast Rad9 checkpoint protein is subjected to
Mec1/Tell-dependent hyperphosphorylation and interacts with Rad53
after DNA damage.",
EMBO J. 17:5679-5688 (1998).

-i- FUNCTION: Essential for cell cycle arrest at the G2 stage
following DNA damage by X-irradiation or inactivation of num
ligase.
                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMMI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-89313732; PubMed=2664461; Schiestl R.H., Reynolds P., Prakash S., Prakash L.; Schiestl R.H., Reynolds P., Prakash S., Prakash L.; "Cloning and sequence analysis of the Saccharomyces cerevisiae RAD9 gene and further evidence that its product is required for cell cycle arrest induced by DNA damage."; Mol. Cell. Biol. 9:1882-1896(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAD9_YEAST STANDARD; PRT; 1309 AA. P14737; 004920; 01-APR-1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
EMBL; M26049;
EMBL; Z48612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Murphy L., Harris D.,
Submitted (MAR-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YEAST
                                                                                                                                                                                                                               -!- SUBUNIT: Physically associates with RAD53.
                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION, AND INTERACTION WITH RAD53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of RAD9 of Saccharomyces cerevisiae and evidence that its function acts posttranslationally in cell cycle arrest after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA repair protein RAD9.
RAD9 OR YDR217C OR YD9934.02C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weinert T.A., Hartwell L.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91061763; PubMed=2247073;

    -!- SIMILARITY: Contains 1 BRCT domain.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 ELCDWDLTGFLNFP 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 LPAKTEW-----IQFAAEN--TKPEVTKPVSEEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QHGRWQARI--GRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNEDISRYDVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMASSNLLAGELARRKKOND-PRNKDIDYNKSVVTSV-NNEETVQVQAG-----NNNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. 10:6554-6564(1990)
AAA34954.1; -.
CAA88497.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Barrell B.G., Rajandream M.A.; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KKHYRGV-RQR
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SOTTING CORRESPONDENT OF THE C

-GNVFDKCIFVLTSLFENREELR 1017

II)

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Query Match
Best Local S
Matches 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0000074; P:regulation of cell cycle; IGI. InterPro; IPR001357; BRCT.
Pfam; PF00533; BRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphorylation; 3D-structure.

DOMAIN 994 1122 BRCT.

CONFLICT 433 433 C -> S (IN REF. 3).

SEQUENCE 1309 AA; 148413 MW; 6B77D39A95021FB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50172; BRCT; 1.
Cell cycle; DNA damage; DNA replication inhibitor; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; S0002625; RAD9.
GO:0005634; C:nucleus; IC.
GO:0005515; F:protein binding; IDA.
GO:0000077; P:DNA damage response, signal transduction re. . .; IMP
GO:00006289; P:nucleotide-excision repair; IMP.
GO:0045944; P:positive regulation of transcription from P. . .; IMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1K3Q; 05-DEC-01.
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                                                                                                                                                                                                                                                                                               347
                                                                                                                                                447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 SNSSPIPKEKD------TFNIHEREVETNNVFSNDIONSSNAATRODIIIAGSSDF 553
547 MNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 VPTTFYMSPSQSHLSNFGMCYGVGENGNFHSPLTVMPLKSDGSLCILEALKRSQTQVMVP 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00292;
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                                     RKSMTNVLSPKKHTDDEKDINTHTEVYNNEIESSSEKKEIV-KKDSRDALAEHAGAPSLL
                                                                                                                                              KFRGANAVINFDISRYDVERIMASSNILAGELARRKK---DNDPRNKDIDY
                                                                                                                                                                                    WIYFETGRSLTKDEDIYYLDIRIGDAVTFDGNEYVVVGLECRSHDLNIIRCIRGYDTVHL 872
                                                                                                                                                                                                                      SIY----RGVTRHHQHGRWQARIGRVA---GNKDLYLGTFSTQEE-----AAEAYDVAAI 446
                                                                                                                                                                                                                                                         ADNSFLSKDDIIFGNAVWCQYT-WNYKFYPGILLEVDTNQD-----
                                                                                                                                                                                                                                                                                               YDLAALK----YWGPSTHINFSIENYQ----VQLEEMKNMSRQEYVAHLRRKSSGFSRGA 398
                                                                                                                                                                                                                                                                                                                                 EENRSTKTSPTKHLKRNSDLDAASIKREPSCSITIQTGETGSGKDSKEQSYVFPE-GIRT 770
                                                                                                                                                                                                                                                                                                                                                                                                        QDGTES--LDVALIEHESKGQSSELQKNLMQLFPSESQEIIQNRRTIKRRQKDTIEIGEE 711
                                                                                                                                                                                                                                                                                                                                                                                                                                            PSGTDSVAVDAKKRGHAKLGOKOPVHRKSIDTF---GORTSOYRGVTRHRWTGRYE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLQTSPKKLVVEEETLME--IKKSKGN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNWVAPTREFSTHQQVLEQQMNCGMGNERNGVSLGSVGCGELQSLSLSMSPGSQSSCVTA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEQKEITDRIYLQLSGKQISDSGSDETERMSPNELDTKKESTIMSEVELTQELPEVEEQQ 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RQQGHMSVQTHPYYSG---LACHGLYQ----APLEEETTKETHVS---DCSSLMPQMTEGL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSS---PKLEDFLGGATMGTHEYGSHERGLSLDSIYYNS-QNAEAQPNRDLL----SQPF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKTQIINSPEQNAL------NATFETPVTLSRINFEPILEVPETSSPSKNTMSKP
                                                                                                            KKKNASGL----LGKRTLIKALSSISLDLSEWAKRAKIILEDNEKNKGDAYRYLRHPIRG 928
                                                                                                                                                                                                                                                                                                                                                                    -----GQTRKGRQVYLGGYDMEEKAARA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 103; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRCT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.6%;
                                                                         TSVNNEETVQVQAGNNNNENDSEWKMVLFNHPSQQQQANGNGSDQKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 127.5; D
Pred. No. 0.82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269; Indels 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLQLHDDNKECNSDK 653
                                                                                                                                                ----- 494
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ATRX PANTR
ID ATRX 1
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 DOMAIN
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-!- FUNCTION: Could be a global transcriptional regulator. Modifies gene expression by affecting chromatin. May be involved in brain development and facial morphogenesis.
-!- SUBUNT: Probably binds EZHS. Binds annexin V in a calcium and phosphatidylcholine/phosphatidylserine-dependent manner (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATRX PANTR STANDARD; PRT; 2492 AA.
Q7YQN4;
L5-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Transcriptional regulator ATRX (X-linked helicase
                                                                                                                                                                                                                                                                                           Pfam; PF00271; helicase C
Pfam; PF00176; SNF2 N; I.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22763540; PubMed=12777533;
Kitano T., Schwarz C., Nickel B., Paabo S.;
"Gene diversity patterns at 10 X-chromosomal loci in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATRX
                                                                                                                                                                                                                                                                                                                                              InterPro; IPRO01410; DEAD.
InterPro; IPRO01650; Helicase_C.
InterPro; IPRO01330; SNP2 N.
Pfam; PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nuclear protein) (XNP).
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB102642; BAC81111.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chimpanzees."
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                                                                                                                                                                                                                                                         Zinc-finger.
                                                                                                                                                                                                                                                                             DNA repair;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SUBCELUUAR LOCATION: Nuclear. Associated with pericentromeric heterochromatin during interphase and mitosis, probably by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1018
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                                                           1151
1166
1202
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1443
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1499
                                                                                                                                                                                                                                                                               Nuclear
                                                                                                                                                                                                      268
1601
1722
                                     1156
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                                                       POLY-SER.
POLY-LYS.
POLY-SER.
POLY-SER.
POLY-SER.
POLY-ASP.
POLY-GLU.
POLY-GLU.
                     POLY-SER.
                                                                                                                                                                                                                         PHD-TYPE.
                                                                                                                                                                                                                                                                             DNA-binding; Helicase; ATP-binding;
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RESULT 13

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DT 01-OCT
DT 15-MAR
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SEQUENCE
                                                                                                                                                                                                           01-NOV-1990 (Rel. 16, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Non-receptor tyrosine kinase spore lysis A (EC 2.7.1.112) (Tyrosine-protein kinase 1).
SPLA OR PYKA OR DPYKI.
MEDLINE=97053827; PubMed=8898241;
Nuckolls G.H., Osherov N., Loomis W.F., Spudich J.A.;
"The Dictyostelium dual-specificity kinase splA is essential for spore differentiation.";
Development 122:3295-3305(1996).
                                                                                           STRAIN=JH10
                                                                                                                                                                        Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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P18160;
                                                                                                                SEQUENCE FROM N.A.
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117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QKIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSRE 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFDTKKGKSAKSSIISKKKR----QTQSESSNYDSELEKEIKSMSKIGA---ARTTKKRI 841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPLRRPTETNPVTSNSDEECNETVKEKQKLSVPVRKKD-----KRNSSDSAIDNPK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNPKLE------KCGLGQENSDNEHLVENEVSL-----LLEESDLRRSPRVKT 661
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2492
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85; Mismatches 218; Indels 182;
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484 DNDPRIKDIDYNKSVYTSYNNEETYQYQAGININIENSEEWKNYLFRIESQQQQAIGIGSD 543

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Query Match
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SMART; SM00449; SPRY; 3.

SMART; SM00449; SPRY; 3.

PROSITE; PS00107; PROTEIN KINASE DOM; PROSITE; PS50011; PROTEIN KINASE DOM; PROSITE; PS00109; PROTEIN KINASE TYR; PROSITE; PS50105; SAM_DOMĀIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email.to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tyrosine phosphate.

-! DEVELOPMENTAL STAGE: Expressed throughout development with a peak during the mound stage of morphogenesis.
-!- SIMILARITY: Belongs to the Tyr family of protein kinases.
-!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                                                                              SEQUENCE
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DOMAIN
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ProDom; PD000001; Prot_kina
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InterPro; IPR001660; SAM.
InterPro; IPR001877; SPRY_receptor.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase_AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U32174; AAB41125.1; -. EMBL; M33785; AAA33202.1; -.
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-!- FUNCTION: Essential for spore differentiation.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyostelium discoideum. Mol. Cell. Biol. 10:3578-
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SEQUENCE OF 1248-1584 FROM N.A.
MEDLINE=90287147; PubMed=1972546;
Tan J.L., Spudich J.A.;
The velopmentally regulated protein-tyrosine kinase genes in
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    Similarity 23.9
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                        3.5%; Score 122;
23.9%; Pred. No. 2.
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                                                                                         ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
D -> R (IN REF. 2).
V -> L (IN REF. 2).
WW; 5D1589458D8E01E3 CRC64;
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CCT1_PANTR
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                                                                                                      PROSITE; PS00292; CYCLINS; FALSE_NEG.
(Cyclin; Cell cycle; Cell division; Coiled coil;
W Transcription, regulation; Nuclear protein.
T DOMAIN 252 269 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
POWAIN 383 424 COILED COIL (POTENTIAL).
DOMAIN 383 424 COILED COIL (POTENTIAL).
DOMAIN 383 424 COILED COIL (POTENTIAL).
DOMAIN 516 529 POLY-HIS.
DOMAIN 516 529 POLY-Rep
DOMAIN 716 724
SEQUENCE
Query Match
Best Local S
Matches 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDM9/cyclin T) complex, also called positive transcription (CDM9/cyclin T) complex, also called positive transcription elongation factor B (P-TEFB), which is proposed to facilitate the translition from abortive to production elongation by phosphorylating the CTD (carboxy-terminal domain) of the large subunit of RNA polymerase II (RNAP II). Binds also to the transactivation domain of the HIV-1 nuclear transcriptional activator, Tat. It is probably the cis-acting transactivation response element (TAR) RNA-binding cofactor for Tat. Also serves as an essential cofactor for HIV 2-Tat and similan immunodeficiency virus (African mandrill) Tat function.

1. SUBCUNIT: Associates with CDM9 to form P-TEFB. Cyclin T1 is the predominant cyclin associated with CDM9 (By similarity).

1. SUBCELIULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22328476; PubMed=12441807; Rollman E.N., Lund L.H., Sjostrand D.E., Leitner T., Wahren B.E.; "A unique amino acid deletion in the chimpanzee cyclin Tl does no affect Tat trans-activation of HIV.";
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NESEPSLPTMAQMPGHSSDTSGL
                         TSWLPS-PTVOMRPSPAISLSHL
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RESULT 15

APC HUMAN STANDARD; PRT; 2843 AÅ.

ID APC HUMAN STANDARD;

AC P25054; Q15162; Q15163;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Adenomatous polyposis coli protein (APC protein)

APC OR DP2.5.

CS Homo sapiens (Human).

CS Homo sapiens (Human).

CC Mammalia; Eutheria; Primates; Catarrhini; Homin

CM MARCHARD STANDARD (N.A.

NCBI TAXID=9606;

RN [1]

RN SEQUENCE FROM N.A.

RX MEDLINE=91335210; PubMed=1651562;

RX MEDLINE=91335210; PubMed=1651562;

RX MEDLINE=91335210; PubMed=1651562;

RX MEDLINE=91335210; PubMed=1651562;

RX Horii A., Smith K.J., Preisinger A.C., Hedge RA Horii A., Ando H., Miyoshi Y., Miki Y., Nishis RT "Identification of FAP locus genes from chromo RL Science 253:661-665(1991).
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MEDLINE=91335210; PubMed=1651562;

Kinzler K.W., Nilbert M.C., Su L.-K., Vogelstein B., Bryan T

Kinzler K.W., Nilbert M.C., Su L.-K., Hedge P., McKechnie

Levy D.B., Smith K.J., Preisinger A.C., Hedge P., McKechnie

Finniear R., Markham A., Groffen J., Boguski M.S., Altschul

Horii A., Ando H., Miyoshi Y., Miki Y., Nishisho I., Nakamur

"Identification of FAP locus genes from chromosome 5q21.";

science 253:661-665(1991).
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Day C.L., Alber T.;
"Crystal structure o
APC tumor suppressor
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MEDLINE=94154728; Pub
Nagase H., Nakamura Y
"Mutations of the APC
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Fisher
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Hamilton S.R., Liu B., Parsons R.E., Papadopoulos N., Jen J. Powell S.M., Krush A.J., Berk T., Cohen Z., Tetu B., Burger Wood P.A., Taqi F., Booker S.V., Petersen G.M., Offerhaus G. Tersmette A.C., Giardiello F.M., Vogelstein B., Kinzler K.W. "The molecular basis of Turcot's syndrome.";
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"Association of the APC tumor suppress
Science 262:1734-1737(1993).
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"A germline mutation at the extreme 3-prime end of the Presults in a severe desmoid phenotype and is associated overexpression of beta-catenin in the desmoid tumor."; Clin. Genet. 57:205-212(2000).
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                                                                                                                                                                                                                                                                                                                                  MEDLINE=21564054; PubMed=11707392;
Eklof Spink K., Fridman S.G., Weis W.I.;
"Modecular mechanisms of beta-catenin recognition by adenomatous
polyposis coli revealed by the structure of an APC-beta-catenin
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MEDLINE=20384842; PubMed=10926498;
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A., Barber
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Biol. 301:147-156(2000)
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Barber J., du Boulay C., Primrose J., Burn J.,
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             the APC (a
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MEDLINE-93265030; Pu...

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Qy . 4 INESNNTDDGNNHNWLGESLSPHWKMEATSAATVPTTFYMSPSQSH 49	Query Match 39.1%; Score 1370.5; DB 10; Length 639; Best Local Similarity 46.6%; Pred. No. 1.6e-90; Matches 337; Conservative 68; Mismatches 169; Indels 149; Gaps 3	-	SMART; SM00380; AP2; 2.	ProDom;	PRINTS;	InterPro; IPR00	GO:0003700; F:transcription factor activity; IEA.	GO; GO:0005634; C:nucleus; IEA.	_		Sasaki T., Matsumoto T., Katayose Y.;	STRAIN=cv. Nipponbare;	RP SEQUENCE FROM N.A.		OC Ehrhartoideae; Oryzeae; Oryza.	Ħ	GN P0474G09.16.	DE Putative ovule development protein antitegumenta (ANT).	01-OCT-2003 (TrEMBLrel. 25, Last annotation updated	01-JUN-2003 (TrEMBLrel. 24,	01-JUN-2003 (TrEMBLrel. 24, Creat	ID Q84Z02 PRELIMINARY; PRT; 639 AA.	Q84Z02 ·	
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Wing R.A., Yu Y., Soderlund C
Saski C., Henry D., Oates R.,
"Rice Genomic Sequence.";
submitted (APR-2002) to the EI
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"Rice Genomic Sequence.";

"Rice Genomic Sequence.";

Submitted (DEC-2002) to the EMBL/G

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GO; GO:0005634; C:nucleus; IEA.

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                                                                                                                                                                  SRYDVERIMASSNLLAGELARRKK-----DNDPRNKDIDYNKSVVTSVNNEETVQVQAG
                                                                                                                                                                                                    IYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDIAAIKFRGLNAVTNFDI
                                                                                                                                                                                                                      IYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDI
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                GTSVTS---WLPSPTVQ----
                                                                VGSGQHNMLDESSKI-GTHFSNTSSLVTSLSSSREASPEKRGPSLLFPMPPMETKIVNPI
                                                                                                                          NNNNENDSEWKKYVLFNHPSQQQQA----NGNGSDQKIMNCGNYRNSAFSMALQDLIGIDS
                                                                                                                                                       TRYDVDKIMESSSLLPGEAARKVKAIEAAPDHVPIGREL-----GATEEASAATVTG
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AVSLAAMNEWMEMPAPAAAHVMREESAI --AHLEVEAAWID
                                                 ESAAADEIDVPGGKISGINFSNSSSLVTSLSNSREGSPERLGLAMLYAKH--
                                                                                                   -TDWRMVL--HGSQQQQAAACTEATADLQK-----GFMGDAHS
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Pred. No. 4.3e-88;
52; Mismatches 146;
               -MRPSPAISLSHLPVFASWTD
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transcription, DNA-dependent;
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CKC.
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SMART; SM00380; AP2;
SEQUENCE 555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005700; F:transcription factor activity; IEA.
GO; GO:0003700; F:transcription of transcription, DNA-dependent;
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
InterPro; IPRO01471; TF ERF
Pfam; PF000847; APZ-domain; 2.
PRINTS; PR00367; ETHRSPELEMNT.
PRODON PRO01423; TF ERF; 2.
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Submitted (DEC-1995) to
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14; Conservative
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                                                                                                                                                                                                                    DLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNLLAGELARRKKD
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SPEKRGPSL--LFPMPPMETKIV-NPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWT
                                                                                                                                                                        NDPRNKDIDYNKSVVTSVNNEETVQVQAGNNNNENDSEWKWVLFNHPSQQQQANGNGSDQ
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                                                                                      KIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREA
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61741 MW;
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to the EMBL/GenBank/DDBJ
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); Mismatches 11
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Pred. No. 1.
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SEQUENCE FROM N.A.

Chan M.M., Chang C.H., Chang E., Dale J.M., Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Quach H.L., Deng J.M., Goldsmith A.D., Lee J.M., Onddera C.S., Quach H.L., Deng J.M., Foriumi M., Mu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., M.H.C., Yamamura Y., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.J., Sakurai T., Satou Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou Saki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker Saki M., Shinn P.,
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01-NOV-1996 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sanctation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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development protein AINTEGUMENTA).
AINTEGUMENTA OR T28119.30 OR AT4G37750.
Arabidopsis thallana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core euerosids II, Brassicales; Brassicaceae; Arabidopsis.
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SEQUENCE FROM N.A.
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Elliott R.C., Betzner A.S.,
Gerentes D., Perez P., Smyt
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Smyth D.R.;
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   Mewes H.W., Mayer K.F.X.,
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Best Local S
Matches 314
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EMBL; U4139; AAB17364.1; ...
EMBL; U4139; AAB17364.1; ...
EMBL; AL0256; AAA81040.1; ...
EMBL; AL161592; CAB80440.1; ...
EMBL; AL161592; CAB80440.1; ...
EMBL; AY1080706; AAL85024.1; ...
EMBL; AY117207; AAM51282.1; ...
PIR; S71365; S71365.
TRANSFAC; T02639; ...
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0006555; P:regulation of tr
InterPro; IPR001471; TF_ERF.
InterPro; AND-4078171; TF_ERF.
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PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF ERF; 2.
SEQUENCE 555 AA; 61725 MW;
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314; Conserv
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                                                    SPEKRGPSL--LFPMPPMETKIV-NPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWT
                                                                                                           KIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLYTSLSSSREA
                                                                                                                                                          DPRNKDIDYNKSVVTSVNNEFTVQVQAGNUNNENDSEWKWVLFNHPSQQQQANGNGSDQ
                                                                                                                                                                                                                                        <u>AENYQKETEDMKNMTROEYVÄHLRRKSSGFSRGASTYRGVTRHHOHGRWOARTGRVAGNK</u>
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Pred. No. 1.5e-87;
9; Mismatches 113;
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transcription, DNA-dependent;
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GO; GC:000534; C:nucleus; IEA.
GO; GC:0003700; F:transcription f
GO; GO:0003700; F:transcription of t
InterPro; IPR001471; TF_BR:
Pfam; pF00847; AP2-domain; 2.
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_BRF; 2.
SNART; SM00380; AP2; 2.
SSEQUENCE 692 AA; 71515 MW; 4D
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STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto
"Oryza sativa nipponbare(GA3) geno
clone:P0035F12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P0035F12.3.
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
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63; Conservative 100;
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GANAVTNFDISRYDVERIMASSNLLAGELARRKKDNDPRNK-DIDYNKSVVTSVNNEETV
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                                                                                                               KSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDIAAIKFR
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A Boutiller K., Offringa R., Sharma V.K., Kieft H., van Lammeren A.A

A Quellet T., Zhang L., Hattori J., Liu C., M., Miki B.L.A.,

Custers J.B.M., van Lookeren Campagne M.M.;

"Ectoptic expression of the Brassica napus BABY BOOM gene triggers in the English and the English growth.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AR317907; AAM31803.1; -.

REMBL, AR317907; AAM31803.1; -.

REGO; GO:0005634; C:nucleus; IEA.

RO; GO:000555; Piregulation of transcription, DNA-dependent; IEA.

RO; GO:0006355; Piregulation of transcription, DNA-dependent; IEA.

RO; GO:0006355; Piregulation of transcription, DNA-dependent; RA;

RO; GO:000637; AR2-domain; 2.

R Pfiam; PR00367; BTHRSPELEMNT.

R BODOM; PD001423; TF_ERF; 2.

R BOART; SM00380; AP2; 2.
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 260; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8LSN1;
01-OCT-2002
01-OCT-2002
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress; Embryophyta; Eukaryota; Viridiplantee; Strophyta; Embryophyta; core eu Spermatophyta; eagnoliophyta; eudicotyledons; core eu eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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[_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTSSLVTSLSSSREASPEKRGPSLLFPMPPMETKIV--NPIGTSVTSWLPSPTVOMRPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDOKIMNCG--NYRNSAFSMALQDLIGIDSV-----GSGQHNML---DESSKIGTHFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVQAGNINNENDSEWKWVLFN-----
                                             MPQMTEGLKNWVAPTRE-FSTHQQVLEQQMNCGMGNERNGVSLG---
                                                                                                                                                 VAGGYCFDLAAPSDESSAVQTSFLSPFGVTLEAF-----
                                                                                                                                                                                    SDGSLCI-LEALKRSQTQVMVPTSSP---KLEDFLGGATMGTHEYGSHERGLSLDSIYYN
                                                                                                                                                                                                                                                        HUMLGFSLSPHMKMEATSAATVPTTFYMSPSOSHLSNFGMCYGVGENGNFHSPLTVMPLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QDLHHLNLGAAAAHDFFSQAMQQQHGLGSIDNASLEHSTGSNSVVYNGDNGGGGGGYIM
                                                                                                              SQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEBTTKETHVSDCSSL
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            QNGPKLENFLGRTTTIYNTNETVVDGNGDCGGGDGGGGGS
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ilarity 36.2%;
Conservative
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                       Score 953; DB 10;
Pred. No. 2.2e-60;
5; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                               1EA3DCDF1C900FB8 CRC64;
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Best Loc
Matches
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Boutilier K., Offringa R., Sharma V.K., Kieft H., van I
Boutilier K., Offringa R., Et al. C.-M., Miki B.L./

Zhang L., Hattori J., Ouellet T., Liu C.-M., Miki B.L./

Custers J.B.M., van Lookeren Campagne M.M.;

"Ectopic expression of the Brassica napus BABY BOOM ger

conversion from vegetative to embryonic growth.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ database;

R EMBL; AF317905; AAM33801.1; -.

R EMBL; AF317905; AAM33801.1; EA.

R GG; GG:0005355; P:transcription factor activity; IEA.

R GG; GG:0006355; P:regulation of transcription, DNA-dep.

R GG; GO:00063700; F:transcription factor activity; IEA.
                                                                                                                       InterPro; IPR001471; TF ERF.
Pfam; PF00847; AP2-domain; 2.
PRINTS; PR00367; ETHRSPELEMNT.
PRODOm; PD001423; TF ERF; 2.
SMART; SM00380; AP2; 2.
SEQUENCE 579 AA; 64018 MW; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002
01-OCT-2002
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brassica napus (Rape).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AP2/EREBP
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                      Match
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                                                                       Similarity
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NHNWLGFSLSP----HMKMEATSAATVPT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYNARNHYYYAQHQQQQIQQSPGGDFPVAISNNHSSNMYFHGEGGGEGAPTFSVWNDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T--HFSNTSSLVTSLSSSREASPEKRGPSLLFPMPPMETKIVNPIGTSVTSWLPSPTV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02 (TrEMBLrel. 22, Created)
02 (TrEMBLrel. 22, Last sequence update)
03 (TrEMBLrel. 24, Last annotation update)
transcription factor BABY BOOM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQQQANGNGSDQKIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIG
                                                                     27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65;
                                                     Score 947; DB 10;
Pred. No. 5.9e-60;
5; Mismatches 155;
                                                                                                                           6426D3B2B06D3BEA
                                                                                                                                                                                                                            factor activity; IEA.
transcription, DNA-dependent;
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                  -TEXMSPSOSHLSNEGMCXGV
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                                                                                        Length
                                                         Indels
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                                                                                                                                                                                                                                                                                                                                 triggers
                                                         158;
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                                                         Gaps
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A Boutlier K., Offringa R., Sharma V.K., Kieft H., van Lammer A Duellet T., Zhang L., Hattori J., Liu C.-M., Miki B.L.A., A Custers J.B.M., van Lookeren Campagne M.M.;

T'Estopic expression of the Brassica napus BABY BOOM gene tri conversion from vegetative to embryonic growth.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF317904; AAM33800.1; -.

R EMBL; AF317904; AAM33802.1; -.

R GO; GO:0005354; C:nucleus; IEA.

R GO; GO:0005555; P:regulation of transcription, DNA-dependent R InterPro; IPR001471; TF_ERF.

R Pfam; PF00847; AP2-domain; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassica napus (Rape).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta,
Spermatophyta, Magnoliophyta, eudicotyledoma, core er
eurosids II, Brassicales, Brassicaceae, Brassica.
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01-OCT-2002 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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22, Last sequence update)
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                                                                QGVDLSLLHQHQERYNG
                                                                                                                                                                                                  AR I GRVAGNKDLYLGT FGT QEEAAEAYD I AAI KFRGLT AVTNF DMNRYNVKAI LESPSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
SNTOSLMTNIDHOSSVSDD
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                                                                 --YYYNGGNLSSESÁRACFKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 942; DB
Pred. No. 1.4e-
61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EA2AFE4734500D72
 492
                                 607
                                                                                                                                   ANR PVPSMMISNNVSESENSASGWQNAAVQHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GDG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TFYMSPSQSHLSNFGMCYGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LRNQPVDNVDNQENG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -sgsgcyg----
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                                                                   473
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Q9CAH3
Q9CAH3;
Q1_JUN_2001 ()
Q1_JUN_2001 ()
Q1_JUN_2003 ()
Putative AP2 ()
F28P22.24.
                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
SEQUENCE FROM N.A.
STRAIN=CV. Columbia;
MEDLINE=201016719; PubMed=11130712;
Theologis A., Ecker J.R., Palm C.J.,
                                                                                           NCBI_TaxID=3702;
                                                                                                                                                                                                                               (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                  domain
                                                                                                                                                                                                                  transcription
                                                                                                                                                                                                                     factor.
    Federspiel
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  N.A.,
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eudicots; rosi
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PRT;

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RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskala I., Kwrtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskala I., Kwrtz D.B., Kwan A., Lam B.,
RA Langin-Hopper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu Z.N., Luros J.S., Maiti R., Marziali A.,
RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
Thaliana.",
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Best Local S
Matches 214
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001471; TF ERF.
Pfam; PF00847; AP2-domain; 2.
PFINTS; PF00847; AP2-domain; 2.
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PR001423; TF ERF; 2.
SMART; SM00380; AP2; 2.
SMART; SM00380; AP2; 2.
SMART; SM00380; AP2; 2.
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PIR; B96750; B96750.
GO; GO:0005634; C:nuc
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                                                                                                                                                                                                                                                                                    170
                                                                     343
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AC010926; AAG51860.1;
403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MPLKSDGSLCILEALKRSQTQVMVPTSSPKLEDFLGGATMGTHEYGSHERGLSLDSIYYN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WLGFSLSPHMKM-----EATSAATVPTTFYMSPSQSHLSNFGMCYGVGENGNFHSPLTV 71
                                                                   SVDSYGQRTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRRGRQAKIGGYDEEEKAARAY
                                                                                                                                                                                                                                    SIDTFGORTSQYRGYTRHRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAY
                                                                                                                                                                                                                                                                                                                                                                                                MPQMTEG------LKNWV---APTREFSTHQQVLEQQMNCGM---GNERNGVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                   QTNVNCTTVVNRLNPP----GYL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETTKETHVSDCSSL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDINFOH-----HHHDEDV-----PKVEDLLS-----NSHQTEYPIN---HN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WLGFSLTPPLRICNSESEELRHDGSDGTLFF------
                                    MASSNLLAGELAR
                                                                                                                                            DLAALKYWGPTTHLNFPLSNYEKEIEELNNMNRQEFVAMLRRNSSGFSRGASVYRGVTRH
                                                                                                                                                           NGSM-----LSLALSHGACSDLINESNVSARVEEPVKVDEKRKRLVVKPQVKESVPRK
                                                                                                                                                                                                                                                                                                               -GSVGCGELQSLSLSMSFGSQSSCVTAFSGT----DSVAVDAK-KRGHAKLGQKQFVHRK
                                                                                                                                                                                                                                                                                                                                                              DPNLSNDYGGFERVGSVSVFKSWLEQGTPAFPLSSHYVTEEAGTSNNISHFSNEETGYNT
CSSSTIVDSDQAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.4%; Score 923.5; DB 1
43.4%; Pred. No. 1.9e-58;
tive 60; Mismatches 108
                                    480
 415
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Best Local S
Matches 253
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Taintegumenta-like protein in rice (Oryza sativa).";

Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AY662180; AAL47205.1; -.

R GG; GO:0005634; C:nucleus; IEA.

R GG; GO:0003700; F:transcription factor activity; IEA.

R GG; GO:000370; F:transcription of transcription, DNA-dependent; IEA.

R GG; GO:000375; P:regulation of transcription, DNA-dependent; IEA.

R GG; GO:000375; P:regulation of transcription, DNA-dependent; IEA.

R GG; GO:000370; F:TEAFF.

R Pfam; PF00847; AP2-domain; 2.

R PRINTS; PR00367; ETHRSPELEMNT.

PPODOM; PD001423; TF_ERF; 2.

R SMART; SM00380; AP2; 2.

R SMART; SM00380; AP2; 2.

R SEQUENCE 597 AA; 62198 MW; F856EBC99BADE25B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8LGQ3;
Q8LGQ3;
01-OCT-2002
01-OCT-2002
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ovule development aintegumenta-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 QNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGL--YQAPLEEETTKETHVSDCSS
                                                                                                                                                     491
                                                                                                                                                                                                      318
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                                                                                                                                                                                                                                                                                                         258
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                                                                                                    378
  435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSE-----SGGSGAVVEA-----GAAAAARKSVDTFGQRTSIYRGVTRHRWTGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----MAGGRKEI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TWDÓWLEGTKAMAYALLEESTHÓOATEÓÓWNCCMCNÉLNGASTGSAGCCETÓSTSTSWSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÓPÁ-PÓP-AQALSISMMAGTTTAQGGGAMALLÁGAGERGRTTPASESISTSAHGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SD---GSLCILEALKRSQTQVMVPTSSPKLEDFLGGATWGTHEYGSHERGLSLDSIYYNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNWLAFSLSPQDQ-------LPPSQT------NSTFISAAATTTTA
                                                                                                                                                                                                                                    FSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNILAGELARRKKDNDPRNK
                                                                                                                                                                                                                                                                                                                                    QLZEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGT
                                                                                                                                                                                                                                                                                                                                                                                                                YEAHLMDNSCRREGQTRKGRQ---GGYDKEEKAARAYDLAALKYMGPTTTTNFPVNNYEK
                                                                                                                                                                                                                                                                                                           ELEENKHWTRQEFVASIRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGT
RGWCKQEQDHAVIAAAHSLQDLHHLNLGAAAAAHDFFSQAMQQQHGLGSIDNASLEHSTG
                                                                                                                                                   ----SQQQQ-----ANGNGSDQKIMNCG--NYRNSAFSMALQDLIGIDSV-----GSG
                                                                                                    YDVG---RIASHLGGDGAYAAHYĞHHHKSAAAAWPTIAFQAAAAPPPHAAGLYHPYAQPL
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36.0%; Pred. No. 6.1e
tive 79; Mismatches
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24,
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transcription, DNA-dependent; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -NEEGSGSAGAV------VAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165;
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        494
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Query Match
Best Local S
Matches 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
Ren S.X., Lu G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.,
Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.,
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

SMEL, AL731638; CAED5555.1; -
SMEL, AL731638; CAED5555.1; -
SEQUENCE 655 AA; 67291 MW; D6FCCD0F729A6933 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Fu G., Wang S.Y., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhu F.H., Han B., Feng Q., Hu ang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y.D., Zhang Y.J., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Hong G.F., Zhang K.Q., Guan J.P., Hong G.F., Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrbartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sannotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
OSJNBB0014K14.16 protein (OSJNBb0116K07.8 protein).
OSJNBA0014K14.16 OR OSJNBB0116K07.8.
OTYZA SALÍVA (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7X6D4;
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                                                                            174
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                                                                                                                                                                                                                 APKLENFLDGNSFSDVHGQAAGGYLYSGSAVGGAGGYSNGGCGGGTIELSMIKTWLRSNQ 173
                                                                                                                                                                                                                                                                                     SPKLEDFLGGATM-----GTHEY-----GSHERG-----LSLDSIYYNSQN 134
                                                                                                                                                                                                                                                                                                                                                                                                                              MPLKSDGSLCILEALKR------SQTQVMVPTS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NWLGFSLSGQGNPQHHQNGSPSAA------GDAAIDISGSGDFYGLPTPDAHHIGMA- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NWLGFSLS-----PHMKMEATSAATVPTTFYMSPSQSHLSNFGMCYGVGENGNFHSPLTV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGAGRMPSWAMTPASAPAATSSSDMTGVCHGAQLFSVWNDT 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QHNML---DESSKIGTHFSNTSSLVTSLSSSREASPEKRGPSLLFPMPPMETKIV--NPI 628
MTEGLKNWVAPTREFSTHQQVLEQQMNCGMGNERNGVSLGSVGCGELQSLSLSMSPGSQS
                                                                        SQQQP----SPP--QHADQGMSTDASASSYAC-----SDVLVGSCGG----
                                                                                                                                            AEAOPNRDLLSOPFROOGHMSVOTHPYYSGLACHGLYQAPLEEETTKETHVSDCSSLMPQ 194
                                                                                                                                                                                                                                                                                                                                                          ---GEDAPYGVMDAFNRGTHETQDWAMRGLDYGGGSSDLSMLVGSSGGGRRTVAGDGVGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GISVISWLPSPIVOMRPSPAISLSH-----LPVFASWIDI 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNSVVYNGDNGGGGGGYIMAPMSAVSATATAVASSHDHGGDGGKQVQMGYDSYLVGADAY 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.2%; Score 918.5; DB 10; Length 655; 42.8%; Pred. No. 8.2e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Mismatches 117; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 255
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Q9LF42;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR001471; TF ERF.

Pfam; PF00847; AP2-domain; 2.

PRINTS; PR00367; ETHRSPELEMNT.

ProDom; PD001423; TF ERF; 2.

SMART; SM00380; AP2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ of EMBL; AL391142; CACO1738.1; -
PIR; T51580; T51580.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005700; Firanscription factor activit;
GO; GO:0006355; P:regulation of transcription,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Ovule development protein aintegumenta-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H., Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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187 DCSSIMPQMTEGIKNWVAPTRE-FSTHQQVLEQQMNCGMGNERNGVSIG-
                                                                                                                                                                               127 SIYYNSQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETTKETHVS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255;
                                                                                                          88 NINNNEQNG-
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                                                                                                                                                                                                                                                                                                                        76 SDGSLCI-LEALKRSQTQVMVPTSSP---KLEDFLGGATMGTHEYGSHER-----GLSLD 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 HIWLGESLSPHMKMEATSAATVPTTFYMSPSOSHLSNEGMCYGVGENGNEHSPLTVMPLK 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                   VAGGYCFDLAAPSDESSAVQTSFLSPFGVTLEAF-----TRDNNSHSRDWDINGGACN 87
                                                                                                                                                                                                                                                                                                                                                                                                NNWLGFSLSPH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRVDSPGG----AVDG-----AVPRKSIDTFGQRTSIYRGVTRHRWTGRYEAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64170 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.2%; Score 916.5; 35.2%; Pred. No. 9.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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---SVAAAGGG--GAVVAAESSSSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                      234
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          "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.

RT Sequence features of the regions of 1,081,958 bp covered by seventeen physically assigned P1 and TAC clones.";

Physically assigned P1 and TAC clones.";

PM Res. 5:379-391(1998).

REMBL; AB016891; BAB08476.1; -...

REMBL; AB016891; BAB08476.1; -...

REGO; GO:0003701; Firanscription factor activity; IEA.

REGO; GO:0003701; Firanscription of transcription, DNA-dependent; IEA.

REGO; GO:0003705; P:regulation of transcription, DNA-dependent; IEA.

REGO; GO:0003705; P:regulation of transcription, DNA-dependent; IEA.

REGO; GO:0003701; TF_ERF.

REGO; GO:0003705; P:regulation of transcription, DNA-dependent; IEA.

REGO; GO:0003705; F:REF: 2.

REGO; GO:0003705; P:REF: 2.

REGO; GO:0003705; P:REGO; P:REF: 2.

REGO; GO:0003705; P:REGO; P:REF: 2.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity to unknown protein.
Arabidopsis thaliana (Mouse-ear cress).
Rukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99156233; PubMed=10048488;
Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTV-----LPVFAS 659
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536 -- SYQTAKS-NLSVLHTPVF
                                                       638 SPTVOMRPSPAISLSHLPVF 657
                                                                                                                                                                   578 LDESSKIGTHFSNTSSLVTSLSSSREASPEKRGPSLLFPMPPMETKIVNPIGTSVTSWLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 GNKDLYLGTFSTOEEAAEAYDIAAIKFRGLNAVTNFDISRYDVKSI-ASCNLPVGGLMPK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 NFPISNYESELEEMKHMTRQEFVASLRRKSSGFSRGASMYRGVTRHHQHGRWQARIGRVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 NFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 VTRHRWTGRYBAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 OPNPLAVSEAS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 SNNTDDGNNHNWLGFSLS---PHMKMEATSAATVPTTFYMSPSQSHLSNFGMCYGVGENG
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                                                                                                               HSAAS----INWINNNISS---
                                                                                                                                                                                                                                                                                                                                                                                                  RKKUNDPRNKOIDYNKS-------VVTSVNNEETVQVQAG--NNNNENDSEWKM 525
                                                                                                                                                                                                                              IF-----GFQANPKAEMRPLANFGSDLHNPSPGYAIMPVMQEGENNFGGSFVGSDGYNN
                                                                                                                                                                                                                                                                                   VLFNHPSQQQQANGNGSDQKIMNCG-NYRNSAFSMALQDLI-----GIDSVGSGQHNM 577
                                                                                                                                                                                                                                                                                                                                              PSPATAAADKTVDLSPSDSPSLTTPSLTFNVATPVNDHGGTFYHTGIPIKPDPADHYWSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNKDLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNL-LAGELAR 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLSLDSIYYNSQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETTK
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Pred. No. 1.3e-56;
552
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QSLT37

ID Q9LT37

ID Q9LT37

ID Q9LT37

PRELIMINARY;

PRT; 540 AA.

AC Q9LT37;

PRT 01-CCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-CCT-2000 (TrEMBLrel. 24, Last annotation update)

DT 01-CT-2003 (TrEMBLrel. 24, Last annotation update)

DT 01-UN-2003 (TrEMBLrel. 24, Last annotation update)

DT 01-UN-2003 (TrEMBLrel. 24, Last annotation update)

DT 01-CT-2000 (TrEMBLrel. 25, Last annotation update)

DT 01-CT-2000 (TrEMBLrel. 24, Last annotation update)

DT 01-CT-2000 (TrEMBLrel. 25, Last annotation update)

DT 01-CT-2000 (TrEMBLrel. 24, Last annotation update)

DT 01-CT-2000 (TrEMBLrel. 25, Last sequence update)

DT 01-CT-2000 (TrEMBLrel. 15, Last seq
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RESULT
Q41832
ID Q4
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Best Local S
Matches 238
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription fa
GO; GO:0006355; P:regulation of tr
Interpro; IPR00471; TF_EFF.
Pfam; PF00847; AP2-domain; 2.
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_ERF; 2.
SWART; SW00380; AP2; 7.
SWART; SW00380; AP2; 7.
SEQUENCE 540 AA; 59066 MW; OAC
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MEDLINE=20277480; I
Nakamura Y.;
"Structural analys
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EMBL; AB
Q41832
Q41832;
01-NOV-1996
01-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                 IYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDI
                                                                                                                                                                                                                                                                                                                                                                                           EEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                           QKQPVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDM 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNCGMGNERNGVSLGSVGCGELOSLSLSMSPGSQSSCVTAPSGTDSVAVDAKKRGHAKLG
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                                                                                                                                                                                                                                                                                   NRYDVKAILESSTLPIGGGAAKRLKEAQALESSRKREAEMIALGSSFQYGGGSSTGSGST
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                                                                                                                                                                                                                                                           -----YNKSV-----VTSVNNBETVQVQAGNNNNENDSEWKMVLFNHPSQ-----
                                                                                                                                                                                                                                                                                                        SRYDVERIMASSNI-LAGELARRKKD----NDPRNKDID----
                                                                                                                   TVOMRPSPAISLSHLPVFASWTD
                                                                                                                                                                                         LHQQTNNYLQQQSSQN--SQQLYNAYLHSNPAL--
                                                                                                                                                                                                                                    SSRLQLQPYPLSIQQPLEPFLSLQNND---ISHYNNNAHDSS----SFNHHSYIQTQLH
                                                                                                                                                                GTHFSNTSSLVTSL----
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  (TrEMBLrel.
                                    PRELIMINARY;
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                                                                                                                                                                                                              QQQANGNGSDQKIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKI
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Pred. No. 4e-56
74; Mismatches
 Created)
Last seq
                                                                                                                                                                SSSREASPEKRGPSLLFPMPPMETKIVNPIGTSVTSWLPSP
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                                      PRT;
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transcription, DNA-dependent;
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  sequence update)
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4 bp covered by sixty P1 and TAC
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EMBL; Z47554; CAA87634.1; EA.
PIR; T03638; T03638;
GO; GO:00035634; C:nucleus; IEA.
GO; GO:0003700; F:transcription f:
GO; GO:0006355; P:regulation of t:
InterPro; IPR001471; TF_ERF.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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Orf protein
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406
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Similarity 44.2%;
00; Conservative 4
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                                                                                                                                                                                                                                               AAIKFRGANAVTNFDISRYDVERIM----
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  NNTGSGVMWGATSGAVVGQQDSSSKQGNGYASN
                                                   NNENDS-EW----KMVLFNHPSQQQQANGNGSD
                                                                                                      AAAASQATMPPSEKDYWSLLALHYQQQQEQERQFPASAYEAYGSGGVNVDFTMGTSSGSN
                                                                                                                                                            ELARKKONDPRNKDI - - -
                                                                                                                                                                                                          AAIKFRGLNAVTNLDMSRYDVESILSSDLPVGGGASGRAAAKFPLDSLQPGSAAAMMLAG
                                                                                                                                                                                                                                                                                                                      TASLRRKSSGFSRGASTYRGVTRHHOHGRWOARTGSVAGNKDLYLGTFSTQEBAAEAYDI
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## SUMMARIES

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## ALIGNMENTS

AINTEGUMENTA; ANT-like polypeptide; GmANT1; soybean; transgenic plant; Soybean AINTEGUMENTA-like polypeptide GMANT1. 01-AUG-2002. Glycine max. 21-OCT-2002 ABB79636; ABB79636 standard; protein; 663 19-DEC-2001; 2001WO-US049294. WO200259332-A2 (first entry) 3

He SS, Dotson SB;

21-DEC-2000; 2000US-0257896P.

(MONS ) MONSANTO TECHNOLOGY LLC.

WPI; 2002-599798/64. N-PSDB; ABN84480.

New nucleic acids encoding AINTEGUMENTA-like polypeptides useful in improving agronomic, horticultural, and quality traits of plants, such increased size of plant organs. as

Claim 3; Page 130-133; 169pp; English.

The present sequence is the protein sequence of GmANT1, a newly identified AINTECUMENTA-like (ANT-like) polypeptide of soybean. The sequence is predicted from clone CPR67663 (see ABN84480), which was obtained from a soybean sequence database screening using Arabidopsis ANT as query. Also isolated was clone CPR67628 encoding GmANT2 (see ABR9637). GmANT1 and GmANT2 show homology to ANT in 2 N-terminal AP2 DNA binding domains, but have C-terminal sequences that bear little, if any, homology to ANT although they share conserved segments with each other. The invention provides nucleic acids encoding ANT-like polypeptides comprising, in the N-terminal to C-terminal direction, 2 AP2 DNA binding domains followed by an amino acid subsequence selected from those given in ABB79629-35. ANT-like polypeptides have been identified in soybean,

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The present sequence is the protein sequence of GmANT2, a newly condensified AINTEGUMENTA-like (ANT-like) polypeptide of soybean. The sequence is predicted from clone CPR67626 (see ABN84481), which was cobtained from a soybean sequence database screening using Arabidopsis ANT cas query. Also isolated was clone CPR6763 encoding GmANT1 (see CABS79636). GmANT1 and GmANT2 show homology to ANT although they share conserved segments with each other. Chomology to ANT although they share conserved segments with each other. Creaming in the N-terminal to C-terminal direction, 2 AP2 DNA binding comprising, in the N-terminal to C-terminal direction, 2 AP2 DNA binding comprising, in the N-terminal to C-terminal direction, 2 AP2 DNA binding comprising, and amino acid subsequence selected from those given in ABB79629-35. ANT-like polypeptides have been identified in soybean, crice, cotton and corn (see ABB79636-41). Nucleic acids (see ABN84480-86) cencoding the ANT-like polypeptides can be used in the construction of transgenic plants, sepecially corn, soybean, canola, wheat, cotton, cotton content quality traits, such as increased size of plant organs. These constructs are especially useful for production of ethanol or animal
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                             H--ESKWIVPHVEENAGESGSIGSMAYGDLQSLSLSMSPSSQSSSVTSSHRASPAVVDSV
                                                                                                                                                                           GT-HEY---GSHERGISIDSIYYNSQNAEAQPNRDLLSQPFRQ----QGHMSVQTHPYY
                                                                                                                                                                                                           YGFYYGLEAENVGLYSALPIMPLKSDGSLYGLETLSRSQAQAMATTSTPKLENFLGGEAM
                                                                                                                                                                                                                                  FGMCYGV-GENGNFHSPLTVMPLKSDGSLCILEALKRSQTQVMVPTSSPKLEDFLGGATM
                                                       QVLEQQMNCGMGNERNGV--SLGSVGCGELQSLSLSMSPGSQSSCVT----APSGTDSV
                                                                                                                  SGTACHGLYQAPIEEETTKETHVSDCSSIMPQ-----MTEGIKNWVAPTREE-STHQ
                                                                                                                                               GTPHHYECSATETMPLSLDSVFY-IQPSRRDPNNNQTYQNHVQHISTNQQQQQQELQAYY
                                                                                                                                                                                                                                                                   MKSMENDDNADLNNQNNWLGFSLSPQMHNIGVSSHSQPSSAAEVVPTSFYHHTAP--LSS
   AVDAKKRGHAKLGQKQPVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQT
                                                                                         STIRNHDMIL----EGSKQSQTSDNNNIHVQNMGGDDAVPVPGIKSW--EVRNFQASHA
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                            49.0%; Score 1715;
54.4%; Pred. No. 7
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The present sequence is the protein sequence of OSANT1, a newly identified AINTEGUMENTA-like (ANT-like) polypeptide of rice. The sequence was predicted from a cDNA clone (see ABN84482) obtained from panicle RNA by PCR amplification. OSANT1 cDNA was not amplified from root or leaf RNAs, suggesting tissue-specific expression. Initial OSANT1 clones had been identified in a rice database screening using the newly identified soybean ANT-like polypeptide GMANT1 education and rice ANT-like polypeptide, OSANT2 (see ABS79639), was also isolated. OSANT1 polypeptide shares high homology with Arabidopsis ANT, GmANT1 and GMANT2 at the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rice AINTEGUMENTA-like polypeptide OsANT1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB79638
                                                                                                                                            Claim
                                                                                                                                                                                    New nucleic acids encoding AINTEGUMENTA-like polypeptides useful in improving agronomic, horticultural, and quality traits of plants, s
                                                                                                                                                                                                                               N-PSDB; ABN84482.
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                                                                                                                                                                     improving agronomic, horticultuincreased size of plant organs.
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                                                                                                                                          3; Page 143-146; 169pp; English
                                                                                                                                                                                                                                                                                                 MONSANTO TECHNOLOGY
                                                                                                                                                                                                                                                                       Dotson SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKGRQVYLGGYDMBEKAARAYDLAALKYWGPSTHINESIENYQVQLEEMKUMSRQEYVAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREASPEKRGPSLLFPMPPMETKIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETVQVQAGNNNNENDSEWKNVLFNHPSQQQQANGNGSDQKIMNCGNYRNSAFSMALQDLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATNPNNVNSWDPSPHLR----PALTLPQMPVFAAWTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWTD
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Matches 341; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   terminal AP2 DNA binding domains, shares conserved segments at the N-terminus, and shares conserved segments with GMANT1 and GMANT2, but not with ANY, at the C-terminus. The invention provides nucleic acids encoding ANT-like polypeptides comprising, in the N-terminal to C-terminal direction, 2 AP2 DNA binding domains followed by an amino acid subsequence selected from those given in ABB79629-35. ANT-like polypeptides were identified in soybean, rice, cotton and corn (see ABB79636-41). Nucleic acids (see ABB84480-86) encoding the ANT-like polypeptides can be used in the construction of transgenic plants, especially corn, soybean, canola, wheat, cotton, tomato or potato claimed) having improved agronomic, horticultural or other quality traits, such as increased size of plant organs. These plants are especially useful for production of ethanol or animal feedstuff
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 YMSPSQSHL-----SNFGMCYGVGEN--GNFHSPLTVMPLKSDGSLCILEALKRSQTQ
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                                                             SLSSSREASPEKRGPSLLFPMPPMETKIVNPIGTSVTS---WLPSPTVQ----MRPSPAI
                                                                                                                                                                                                  --- DNDPRNKDIDYNKSVVTSVNNEETVQVQAGNNNNENDSEWKWYLFNHPSQQQA----
                                                                                                                                                                                                                                                      LGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNLLAGELARRKK----
                                                                                                                                                                                                                                                                                                         YRDEIEEMERMTRQEYVAHLRRRSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAAAGDGQGSNSNDGGEQRVGKKRGTGKGGQKQPVHRKSIDTFGQRTSQYRGVTRHRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---LVTSYGACYGNO----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HQLV---PYN-----YQPLTEAEMLQEAAAAPMEDAM-----AAAKNF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HMSVQTHPYYSGLACHGLYQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -MMPSSSPKLEDFLGCGNGSGH------DPATYYSQGQEAED-----ASRAAYQH
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                                                                                                                          NGNGSDQKIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKI-GTHFSNTSSLVT
                                                                                                                                                                  APDHVPIGREL-----GATEEASAATVTG-----TDWRMVL--HGSQQQQAAACT
                                                                                                                                                                                                                                    LGTFSTQEEAAEAYDIAAIKFRGLNAVTNFDITRYDVDKIMESSSLLFGEAARKVKAIEA
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SLSHLPVFASWTD
                                  SLSNSREGSPERLGLAMLYAKH----
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Pred. No. 2.4e-121;
4; Mismatches 149;
                                                                                                    ALHGIVGFDVESAAADEIDVPGGKISGINFSNSSSLVT
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                                  -HPTAVSLAAMNPWMPMPAPAAAHVMRPPSAT
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631 -- AHLPVFAAWTD

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RESULT 4
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acids encoding AINTEGUMENTA-like polypeptides useful in improving agronomic, horticultural, and quality traits of plants, such increased size of plant organs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 154-157; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 669
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Local .
341;
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DB; ABN84483, ABN84484.
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                                                                                                                                                                                                                                                                                                                              h 38.5%; Score 1349.5; DB 5;
Similarity 45.3%; Pred. No. 8e-116;
41; Conservative 66; Mismatches 142;
                                                                                                                                                                                                                                              GGVGGWLGFSLSPHMATYCAGGVDDVGHHHHHHVHQHQQQHGGGLFYNPAAVASSFYYGG
                                                                                                                                                                                                      SQ----SHLSNFGMCYGVGENGNFHSPLTVMPLKSDGSLCILEALK--RSQTQVMVPTSS
                                                                                                                                                                                                                                                                                        GNNHNWLGFSLSPHMKMEAT------45
  GGAVGGDPHHGGGGFLQC--
                                                                                                                       PKLEDFIG-GATMGTHEYGSHERGISLD--SIYYNSQNAEAQPNRDLLSQPFRQQGHM-- 154
                                                                                                                                                                   GHDAVVTSAAGGGSYYGAG
                                       --SVQTHPYYSG---LACHGLYQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREF
                                                                                 PKLEDFLGAGPAM------ALSLDNSAFYYGGHG----
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  NTWASPSPAVSSVPARAGVSIAHLPMFAAWTD
                                      TSWL-PSPTVQMRPSPA-ISLSHLPVFASWTD
                                                                                                                   SKIGTHFSNTSSLVTSLSSSREASPEKRGP-----SLLFPMPPMETKIVNPIGTSV
                                                                                                                                                       AAALPAAARTEQQQQHGHGGHQ---HHDLLPSDAFSV-LQDIVSTVDAAGAPPR-----
                                                                                                                                                                                                                                        ESSTLLPGBLARRKGKVGDGGG------AAAVADAAAALVQAG-----NVAEWKMAT
                                                                                                                                                                                                                                                                                                                       NKDLYLGTFIASAFAAARRARHAGTQEEAAEAYDVAAIKFRGLNAVTNFDITRYDVDKIL
                                                                                                                                                                                                                                                                                                                                                                                                    PPLEDYQEELEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVSG
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                                                                                                                                                                                                  ----FNHPSQQQQANGNGSDQKIMNCGNYRNSAFSMALQDLIG-IDSVGSGQHNMLDES
                                                                              TSLGNSREQSPD-RGVGGGGGGGVLATLFAKPAAASKLYSPV--PL
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AAB07724 standard; protein; 555 AA.

AAB07724;

07-NOV-2000 (first entry)

An Arabidopsis aintegumenta (ANT) polypeptide.

Aintegumenta; ANT; cell proliferation; growth; organ mass; fertility; asexual reproduction; plant; male sterile plant; female sterile plant
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WPI; 2000-465969/40

Fischer RL,

CALIFORNIA.
Mizukami Y;

(REGC )

VIND

08-JAN-1999;

99US-00227421

N-PSDB;

Claim 11;

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The present sequence represents an aintegumenta (ANT) polypeptide. The ANT gene is expressed and functions not only in developing ovules but also in various developing organs. Growth and cell proliferation in plant can be modulated by modulating ANT activity. Modulation of ANT activity is used to alter organ mass, control fertility and enhance asexual reproduction in plants. Increased ANT activity can be used to produce male or female sterile plants. Inhibition of ANT activity can be used to truncate vegetative growth, resulting in early flowering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulating growth and cell proliferation in a plant used to alter organ mass, control fertility and enhance asexual reproduction in plants comprises modulating ANT activity and selecting plants with altered cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA59220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THPYYSGLACHGLYQAPLESETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFLGGATMGTHEYGSHERG--LSLDSIYYNSQNAEAQPNRDLLSQPF----RQQGHMSVQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPSQSHLSNFGMCYGVGENGNFHSPLTVMPLKSDGSLCILBALKRSQTQVMVPTSSPKLE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKSFCDNDDNNHSNTTNLLGFSLSSNMMKMGGRGGREAIYSSSTSSAATSSSSVPPQLVV
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                                               SPEKRGPSL--LFPMPPMETKIV-NPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWT
                                                                                                                                                                                                                KIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREA
                                                                                                                                                                                                                                                                                                                                  NDPRNKDIDYNKSVVTSVMNEETVQVQAGNNNNENDSEWKMVLFNHPSQQQQANGNGSDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AENYOKE I EDMKNMTROEYVAHLRRKSSGFSRGAS I YRGVTRHHOHGRWQARIGRVAGNK
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9; Mismatches 113;
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AAG31380 standard; thaliana protein (first protein; entry) 555 fragment 8 SEQ ID NO:

Protein identification; hybridisation assay; gen genetic signal al transduction pathway; metabolic
mapping; gene expression control; pathway;

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                                                                                                                                               69;
                                                                                                                                             Score 1328; DB 3;
Pred. No. 5.8e-114;
9; Mismatches 113;
                                                                                                                                                                              Length
                                                                                                                                                 Indels
                                                                                                                                                 226;
                                                                                                                                                 Gaps
                                        103
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18-JUN-1999
22-JUN-1999
23-JUN-1999
23-JUN

99US-013945FP.
99US-013945PP.
99US-013945PP.
99US-013946PP.
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99US-014239PP.
99US-0144334PP.
99US-0144334PP.
99US-0144334PP.
99US-014508PP.
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99US-014508PP.
99US-0147302PP.
99US-0147303PP.

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RESULT 7
ABR4082
ID ABR4
XX ABR4
XX ABR4
XX ABR4
XX Flar
DT 16-M
XX Plar
CKW rece
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 (DUPO )
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                                                                                                                                              WO2003002751-A2
                                                                                                                                                                             Arabidopsis thaliana.
                                                                                                                                                                                                             transgenic
                                                                                                                                                                                                                            CKC-like transcription
                                                                                                                                                                                                                                                                                                         Arabidopsis
                                                                                                                                                                                                                                                                                                                                         16-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                        ABR40832 standard;
                                                                                                                 09-JAN-2003
                                                                                 27-JUN-2002;
                                                 29-JUN-2001;
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PIONEER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFLGGATMGTHEYGSHERG--LSLDSIYYNSQNAEAQPNRDLLSQPF----RQQGHMSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STPERLLSFPAIFALPQVNQKMFGSNMGGNMSPWTSNPNAELK-TVALTLPQMPVFAAWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDPRNKDIDYNKSVVTSVNNEETVQVQAGNNNNENDSEWKWVLFNHPSQQQQANGNGSDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>AENYQKEIEDMKNMTRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNK</u>
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                                                                                                                                                                                                                                                                                                         thaliana oil trait related protein sequence
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                                                                                 2002WO-US020152
                                                    2001US-0301913P
     DE NEMOURS & CO
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                                                                                                                                                                                                                              factor;
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kinase;
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Best Local S
Matches 314
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Jones TJ,
Tarczynski
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Allen w Kinney i MC; WB, Cahoon Klein H RE Epelbaum S, Fan Li C, Oliveira Famodu OO, Harvira IC, Sakai H, Harvell LT; Shen B --

Novel nucleotide fragment encoding polypeptides protein kinase activity, caleosin-like activity, phenotypes in plants such as sunflower, coconut, having receptor-like, useful for altering, soybean, wheat and

rice 011

Page 463-465; 542pp; English.

The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a polypeptide (PP) having receptor-like protein kinase activity, mitogen activated protein (MAP)-kinase activity, LIP15-like transcription factor activity and CKC-like activity, ATP citrate lyase activity, NNF1-like activity and CKC-like transcription factor activity. Also described: (1) cc complement (II) of (I); (2) a chimeric construct (III) comprising (I) or (II), operably linked to a regulatory sequence; (3) a plant (IV) cc comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5) cc librained from (IV). (I) or its part can be used in antisense collocation or co-suppression in a transformed plant. (III) is also useful for canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for creating transgenic plants having altered lipid profiles. (I) can also be used as a hybridisation probe. ACC00626 and ABR40591 to ABR40879 represent sequences used in the exemplification of the present

A

Similarity DFLGGATMGTHEYGSHERG--LSLDSIYYNSQNAEAQPNRDLLSQPF----RQQGHMSVQ G---DNTSNFGVCYGSNPNGGTYSHMSVMPLRSDGSLCLMEALNRSSHSNHHQDSSPKVE MKRINESUNTDDGNNHNWLGFSLSPH-MKM---THPYYSGLACHGLYQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLE DFFG----THHNNTSHKEAMDLSLDSLFYNTTH---EPNTTTNFQEFFSFPQTRNH----MKSFCDNDDNNHSNTTNLLGFSLSSNMMKNIGGRGGREAI YSSSTCSAATSSSSVPPQLVV DLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNLLAGELARRKKD HRWTGRYEAHLWDNSFKKEGHSRKGRQVYLGGYDMEBKAARAYDLAALKYWGPSTHTNFS HRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFS QQISEALVETSVGFETTTMAAAKKKRGQEDVVVVGQKQIVHRKSIDTFGQRTSQYRGVTR DLYLGTFGTQEEAAEAYDVAAIKFRGTNAVTNFDITRYDVDRIMSSNTLLSGELARRN--Conservative -GSFNVGV -----PSLTHG 37.9%; -GTDSVAVDAKKRGH---AKLGQKQPVHRKSIDTFGQRTSQYRGVTR ---YGEFQQSLSLSMSPGSQSSCITGSHHHQQNQNQNQNHQSQNH 69; Score 1328; DB Pred. No. 5.8e-69; Mismatches .8e-114 DB ----EATSAATVPTTFYM 9 Length Indels 555; 226; Gaps 60 217 117 103 484 424 349 364 289 304 229 166 405 261

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RESULT 8
ABR40830
IID ABR44
XX ABR44
XX ABR4
XX ABR4
XX ABR4
XX ABR4
XX AFAE
XX WO22
YO 09-0
XX AFAE
X
The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a polypeptide (PP) having receptor-like protein kinase activity, mitogen activated protein (MAP)-kinase activity, LIP15-like transcription factor activity and CKC-like activity, ATP citrate lyase activity, NNF1-like cactivity and CKC-like transcription factor activity. Also described: (1) complement (II) of (I); (2) a chimeric construct (III) comprising (I) or complement (II) in its genome; (4) seeds (V) obtained from (IV); and (5) cc (ii) obtained from (V). (I) or its part can be used in antisense (CC inhibition or co-suppression in a transformed plant. (III) is also useful for CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for CC creating transgenic plants having altered lipid profiles. (I) can also be CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase; receptor-like protein kinase; mitogen activated protein kinase; oil; LIP15-like transcription factor caleosin; ATP citrate Lyase; SNF1; CKC-like transcription factor; antisense inhibition; co-suppression; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Allen
Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering phenotypes in plants such as sunflower, coconut, soybean, wheat and i
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HI-BRED INT INC
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mi H, Shen B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                     AENYQKETEDMKONTRQEYVÄHLRRKSSGFSRGÅSTYRGVTRHHQHGRWQARTGRVÄGNK
                                                                                                                                                                                                                                                                                                                                                                                                                 HRWTGRYEAHLWDNSFKKEGHSRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHTNFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFLGGATMGTHEYGSHERG--LSLDSIYYNSQNAEAQPNRDLLSQPF----RQQGHMSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G---DNTSNFGVCYGSNPNGGTYSHYSVMPLRSDGSLCLMEALNRSSHSNHHQDSSPKVE
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                                                                                                                                                                                                                                                                                                   NDPRNKDIDYNKSVVTSVNNEETVQVQAGNNNNENDSEWKWVLFNHPSQQQQANGNGSDQ
                                                                                                                                                                                                                                                                                                                                     DIYLGTESTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNLLAGELARRKKD
                                                                                                                                                                                                                                                                                                                                                                                                                               HRWTGRYEAHLMDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQISEALVETSVGFETTTMAAAKKKRGQEDVVVVVGQKQIVHRKSIDTFGQRTSQYRGVTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQMNCGMGNERNGVSLGSVGCGEL-QSLSLSMSPGSQSSCVTAPS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THPYYSGLACHGLYQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLE
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                                                                                                                                                                                                             SPEKRGPSL---LEPMPMETKIV-NPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWT
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                                                                                                                                                                                         TALNA-
                                                                                                                                                                                                                                                          KIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREA
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Pred. No. 5.8e-114;
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A Brassica aintegumenta

(ANT)

polypeptide.

Aintegumenta; ANT; cell proliferation; growth;

organ

mass;

fertility;

07-NOV-2000

(first

entry

AAB07725

standard;

protein;

Fischer (REGC )

Modulating

Claim 15;

08-JAN-1999;

VIND

WO200040694-A2

556

465

501 919 496

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The present sequence represents an aintegumenta (ANT) polypeptide. The ANT gene is expressed and functions not only in developing ovules but also in various developing organs. Growth and cell proliferation in plant can be modulated by modulating ANT activity. Modulation of ANT activity is used to alter organ mass, control fertility and enhance asexual reproduction in plants. Increased ANT activity can be used to produce male or female sterile plants. Inhibition of ANT activity can be used to produce truncate vegetative growth, resulting in early flowering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            asexual reproduction; early flowering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JAN-2000; 2000WO-US000465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprises modulating
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                                                                                                                                                                                                                                                                                                                                                                                                                  9 NTDDGNNHNWLGFSLSPHM-----KMEATSAATVPTTFYMSPSQ----SHLSNFGMCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RL, Mizukami
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                         ERNGVSLGSVGCGEL-OSLSLSMSPGSOSSCVTA------P
                                                                                                                                                                                                                                                                                                   TMGTHEYG-SHERG--LSLDSIYYNSQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLA
                                                                                                                                                                                                                                                                                                                                                          GVG-ENGNFHSPLTVMPLKSDGSLCILEALKRS-----QTQVMVPTSSPKLEDFLGGA 109
                                                                                                                                                                                                                                                                                                                                                                                        DNDDSNTTNLLGFSLSSNMLKMGGGEALYSSSSSSVATS--SVPPOLVVGDNSSNYGVCY
                RQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAE
                                                                        CKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNWS
                                                                                                         TTTMAAAAAKKKRGQEVVVGQKQIVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNS
                                                                                                                            SGTDSVAVDAKKRG-HAKLGQKQPVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNS
                                                                                                                                                            ---ĠGŚĘNVGVYĠĖFQQŚĹŚĹŚMŚĖĠŚQŚŚĊIŤASHHHQNQTQNHQQISEALVETSAGFE
                                                                                                                                                                                                                      ------EEET--RNYEND-----PGLTHG------
                                                                                                                                                                                                                                           CHGLYQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLEQQMNCGMGN
                                                                                                                                                                                                                                                                              -FGTHHHNTSHKEAMDLSLDSLFYNTTHA---PNNNTNFQEF----FSFPQTRNHH----
                                                                                                                                                                                                                                                                                                                                  GSNLAAREMYSQMSVMPLRSDGSLCLMEALNRSSHSNNHHHSQV----SSPKMEDF----
RQEYVAHLRRKTSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAAE
                                                     FKKEGHSRKGROVYLGGYDMEEKAARAYDLAALKYWGPSTHTNFSVENYOKEIDDMKNMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 44; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           77;
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Pred. No. 5.1e-112;
7; Mismatches 103;
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05-MAR-1999

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06-APR-1999

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 99US-0121825P.
99US-012548P.
99US-012548P.
99US-0125788P.
99US-0126785P.
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n control;
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promoter;
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Query Match Best Local S Matches 309

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Best Local Simi
Matches 301;
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                                             Protein identification; signal transduction pathway; metabolic
hybridisation assay; genetic mapping; gene expression control;
termination sequence.
                                                                                                                                       AAG31381 standard;
           EP1033405-A2
                           Arabidopsis thaliana
                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 37676.
                                                                                                   17-OCT-2000
                                                                                                                     AAG31381;
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                                                                                                                                                                                                                                                                                                                                                                       QQNQNQNHQSQNHQQISEALVETSVGFETTTMAAAKKRGQEDVVVVGQKQIVHRKSIDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TQVMVPTSSPKLEDFLGGATMGTHEYGSHERG--LSLDSIYYNSQNAEAQPNRDLLSQPF
                                                                                                                                                                                    NILAGELARRKKONDPRNKDIDYNKSVVTSVNNEETVQVQAGNNNNENDSEWKWVLFNHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSFPQTRNH-----PSLTHG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----RQQGHMSVQTHPYYSGLACHGLYQAPLEBETTKETHVSDCSSLMPQMTEGLKNWVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSNHHQDSSPKVEDFFG----THHNNTSHKEAMDLSLDSLFYNTTH---EPNTTTNFQEF
                                                                                                                                                                                                                         ---VVEGGSNKEVSTPERLLSFPAIFALPQVNQKMFGSNMGGNMSPWTSNPNAELK-TVA
                                                                                                                                                                                                                                   SSIVTSLSSSREASPEKRGPSL--LFPMPPMETKIV-NPIGTSVTSWLPSPTVQMEPSPA
                                                                                                                                                                                                                                                                             SQQQQANGNGSDQKIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNT
                                                                                                                                                                                                                                                                                                 TLLSGELARRN-----
                                                                                                                                                                                                                                                                                                                                                                                                            FGQRTSQYRGVTRHRWTGRYEAHLWDNSFKKEGHSRKGRQVYLGGYDMEEKAARAYDLAA
                                                                                                                                                                                                                                                                                                                                                                                                                        FGQRTSQYRGVTRHRWTGRYEAHLMDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.0%;
ilarity 44.6%;
Conservative 6
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5%; Pred. No. 5.6e
63; Mismatches
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6.6e-111;
les 102;
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                                                        promoter;
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                                                                                                                                                                RWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGANAVINFDISRYDVERIMASS
                 HSNHHQDSSPXVEDFFG----THHNNTSHKEAMDLSLDSLFYNTTH---EPNTTTNFQEF
                                                                                                                                                TQVMVPTSSPKLEDFLGGATMGTHEYGSHERG--LSLDSIYYNSQNAEAQPNRDLLSQPF
                                                                 QQNQNQNHQSQNHQQISEALVETSVGFETTTMAAAKKKRGQEDVVVVGQKQIVHRKSIDT
                                                                                          ------GSFNVGV-----YGEFQQSLSLSMSPGSQSSCITGSHHH
                                                                                                PTREFSTHQQVLEQQMNCGMGNERNGVSLGSVGCGEL-QSLSLSMSPGSQSSCVTAPS--
                                                                                                                                                                                        37.0%;
llarity 44.6%;
Conservative 6:
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                                                                                                                                                                                       Score 1295.5; DB 3;
Pred. No. 5.7e-111;
3; Mismatches 102;
                                                                             ----GTDSVAVDAKKRGH---AKLGQKQPVHRKSIDT
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       471
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RESULT 12
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                                                              The present sequence is the protein sequence of GhANT1, a newly identified AINTEGUMENTA.like (ANT-like) polypeptide of cotton. The sequence was predicted from a cDNA clone (see ABN94485) isolated in a cotton DNA database screening. The invention provides nucleic acids encoding ANT-like polypeptides comprising, in N-terminal to C-terminal direction, 2 AP2 DNA binding domains followed by an amino acid subsequence selected from those given in ABB79629-35. ANT-like polypeptides were identified in soybean, rice, cotton and corn (see ABB7963-41). Nucleic acids (see ABN94480-86) encoding the ANT-like polypeptides can be used in the construction of transgenic plants, especially corn, soybean, canola, wheat, cotton, tomato or potato (claimed) having improved agronomic, horticultural or other quality traits, such as increased size of plant organs. These plants are especially useful for production of ethanol or animal feedstuff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acids encoding AINTEGUMENTA-like polypeptides useful in improving agronomic, horticultural, and quality traits of plants, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-599798/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Page 158-161; 169pp; English.
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size of plant organs.
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                                                                                      DSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREASPEKRGPSLLFPMPPMETKIVNP
                                                                                                                                               AGNNNNE-NDSEWKWVLFNHPSQQQ-QANGNGSDQKIMNCGNYRNSAFSMALQDLIGI--
                                                                                                                                                                                 SAVTNEDISKYDVKRICSSSTLIGGELAKKSPKDTASIAPEDYN-SCASSASPOPLLAIP
                                                                                                                                                                                                         NAVTNEDISRYDVERIMASSNILAGELARRKKONDERNKDIDYNKSVVTSVNNEETVQVQ
                                                                                                                                                                                                                                           SGFSRGASVYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDIAAIKFRGT
                                                                                                                                                                                                                                                                   SGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGA
                                                                                                                                                                                                                                                                                                      VYLGGYDKEEKAAKAYDLAALKYWGPTTHINFPLSTYEKELEEMKUMTRQEFVAHLRRKS
                                                                                                                                                                                                                                                                                                                    VYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKS
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 LGN----
                            IGTSVTSWLPSPTVQMRPSPAISLSH-LPVFASWTD
                                                                                                                    SGEASDELADMVWTA---NSDEQQQHQSTNTNNDASLANSSS-RNSSNPQSPKGSIGLAS
                                                                                                                                                                                                                                                                                                                                                               KRPVGKNLTRESVPRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQ
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                                                           --GDYSHHG-YFSLKGSKYEDGNSETDNSNENR-
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   -LGLVHKIPMFALWNE
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Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase; receptor-like protein kinase; mitogen activated protein kinase; oil; LIP15-like transcription factor caleosin; ATP citrate lyase; SNP1; CKC-like transcription factor; antisense inhibition; co-suppression;
             09-JAN-2003
                                                                                                                                                           Glycine max oil trait related protein sequence
                                                                                                                                                                                   16-MAY-2003
                                                                                                                                                                                                            ABR40856;
                                                                                                                                                                                                                                   ABR40856 standard; protein;
                                     WO2003002751-A2
                                                           Glycine
                                                                                   transgenic plant
                                                            max.
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SEQ

ID NO:491

Query Match Best Local

Local Similarity

33.7%; 41.7%;

Score 1180.5; DB 5; Pred. No. 3.4e-100;

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S
                                음 성
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Best Local S
Matches 260
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Jones
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DB; ACC00850.
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13'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260;
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PIONEER HI-BRED INT INC
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                                                   DVAAIKFRGANAVTNFDISRYDVERIMASSNLLAGELARRKKUNDFRNKDI-DYN---KS
                                                                                                                      EYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAY
                                                                                                                                                                    KEGOTRKGROVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNMSRO
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 VVTSVNNEETVQVQAGNNNNE-NDSEWKMVLFNHPSQQQQANGNGSDQKIMNCGNYRNSA
                                                                                                    EFVANLRRKSSGFSRGASVYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAY
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Kinney AJ,
i MC;
                                   DIAAIKFRGTSAVTNEDISRYDVKRICSSSTLIAGDLAKRSPKESPAPVPASDFNSCGSS
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ilarity 43.1%;
Conservative 6
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Klein
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Pred. No. 3.8e-89;
7; Mismatches 125;
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Li C, Oliveira IC, Sakai H, Shen B;
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   The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a CC polypeptide (PP) having receptor-like protein kinase activity, mitogen activated protein (MAP)-kinase activity, LIF15-like transcription factor activity and CKC-like transcription factor activity. Also described: (1) cC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or CC (II), operably linked to a regulatory sequence; (3) a plant (IV) CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5) cll obtained from (IV). (I) or its part can be used in antisense CC inhibition or co-suppression in a transformed plant. (III) is useful for CC allering the oil phenotype in a plant such as corn, soybean, wheat, rice, CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for creating transgenic plants having altered lipid profiles. (I) can also be CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant; oil trait; oil phenotype; altered lipid profile; receptor-like protein kinase; mitogen activated protein LIP15-like transcription factor caleosin; ATP citrate ly CKC-like transcription factor; antisense inhibition; cotransgenic plant.
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                                                                                                                                                                                                                                                 Claim 12; Page 374-376; 542pp;
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N-PSDB; ACC00803.
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                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a CC polypeptide (PP) having receptor like protein kinase activity, mitogen cativated protein (MAP)-kinase activity, LPIS-like transcription factor activity and CKC-like transcription factor activity and CKC-like transcription factor activity. Also described: (1) cc activity and CKC-like transcription factor activity. Also described: (1) cc complement (II) of (I); (2) a chimeric construct (III) comprising (I) or CC complement (II) in its genome; (4) sequence; (3) a plant (IV); and (5) cc comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5) cc oil obtained from (V). (I) or its part can be used in antisense confliction or co-suppression in a transformed plant. (III) is useful for CC campla, Brassica, sorghum, sunflower or coconut. (III) is also useful for creating transgenic plants having altered lipid profiles. (I) can also be used as a hybridisation probe. ACC00626 to ACC00868 and ARR40591 to ACC00868 and ARR40591 to constitution of the present sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 285
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Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 369-371; 542pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering phenotypes in plants such as sunflower, coconut, soybean, wheat and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-201509/19.
N-PSDB; ACC00801.
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QQMNCGMGNERNGVSLGSVGCGELQSLSLSMSPGSQSSCVTAPSGTDSVAVDAKKRGHAK
                                 NSASTDYMFPAQPVSAGGGGSGGGSNNNNNSNSIGLSM---IKTWL-----RNQPPNS
                                                                                                                           flggatmgtheygsherglsldsiyynsqnaeaqpnrdllsqpfrqqghmsvqthpyysg
                                                                                                                                                             SYGIYE --AFHRNNSINTTQDWKENYNSQNLLLGTSCNKQNYNQNQNQQQ------QPKLEN
                                                                                                                                                                                            CYGVGENGNFH---SPLTVMPLKSD-----GSLCILEALKRSQTQVMVPTSSPKLED
                                                                                                                                                                                                                          NLLGFSLSPHEEHPSSQDHSQTTPSRFSFNPDGSISSTDVAGGCFDLTSDSTPHLLNL-P
                                                                                                                                                                                                                                                         NWLGFSLSPHMKMEATS--AATVPTTFYMSP-----
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Kinney AJ,
MC;
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                                                                                                                                                                                                                                                                                                                                                        AA;
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Klein TM,
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Pred. No. 1.4e-
88; Mismatches
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                                                                  KETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLE
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Li C, Oliveira IC, Sakai H, Shen
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.4e-87;
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	LYYLTQQQSSSVDTVKASAYDQGSACNTWVPTAIPTHAPRSTTSMALCH 696	648	D D
	RGPSLLFEMPPMETKIVNPIGTSVTSWLPSPTVQMRPSPAISLSH 653	609	Ş
647	YGGGGGYNVMPMGTTTAVVASDGDQNPRSNHGFGDNEIKALGYESVYGSATDSYHAHARN 647	588	₽ D
608	GSGQHNML	571	Ş
587	QQDNSDAPHSLSYSDIHQLQLGNNGTHNFFHTNSGLHPMLSMDSASIDNSSSSNSVVYDG 587	528	ЪЬ
570	QQANGNGSDQKIMNCGNYRNSAFSMALQDLIGIDSV	535	Ş
527	DHSIIMSSHLTQGINNNYAGGGTATHHNWHNAHAFHQPQPCTTMHYPYGQRINWCKQE	470	ф
534	DYNKSVVTSVNNEETVQVQAGNNNNENDSEWKMVLFNHPSQQ	493	S
469	DVAAIKERGLSAVTNEDMSRYDVKSILESTTLPIGGAAKRLKDMEQVELSVDNGHRADQV	410	Ф
492	DVAAIKERGANAVTNEDISRYDVERIMASSNLLAGELARRKKDNDERNKDI 492	442	Ş
409	EYVASLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAY	350	рb
441	EYVAHLRRKSGGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAY 441	382	8
349	REGOTRKGROVYLGGYDXEEKAARAYDLAALKYWGTTTTTNFFISHYEKELEEMKHMTRO	290	qq
381	KEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNMSRQ	322	Ş
289	SDNKQPNTSAALDSTQTGAIETAPRKSIDTFGQRTSIYRGVTRHRWTGRYEAHLWDNSCR	230	В
321	LGQKQPVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCK	278	8
229	ENINNNNESGGNIRSSVQQTLSLSMSTGSQSS-TSLPLLTASVDNGESS 229	182	Дb

Search completed: March 9, 2004, 10:45:34 Job time: 63 secs

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Listing first 45 summaries
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Perfect score:
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225432109
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192.5
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1: /cgn2_6/ptodata/2,
2: /ggn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-09-27-421-2
US-09-27-421-5
US-09-27-421-5
US-09-27-421-5
US-09-12-72-10
US-08-912-72-10
US-08-912-72-11
US-08-912-72-11
US-08-912-72-11
US-08-912-72-11
US-08-912-72-11
US-08-912-72-1
US-08-912-72-5
US-08-912-72-7
US-08-912-72-7
US-08-912-71-7
US-08-912-71-7
US-09-18-119C-57
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Sequence 10, Appli
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	90	29	28
130.5	131	131.5	132	132.5	132.5	132.5	132.5	132.5	133	133.5	134	134.5	134.5	135	135.5	136	136
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ence 57	equence 59	equence 4,	e 91,	equence 63,	equence 69,	equence 61,	ence 29,	equence 29,	equence 93,	equence 77,	equence 34,	equence	equence 27,	equence 1,	equence	ence 47,	-

## ALIGNMENTS

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Sequence 2, Application US/09227421
Patent No. 6559357
Patent No. 6559357
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Ferl
TITLE OF INVENTION: and Enhancing Asexual Reproduction in Plants
TITLE OF INVENTION UNMEER: US/09/227,421
CURRENT APPLICATION NUMBER: US/09/227,421
CURRENT FILING DATE: 1999-01-08
PRIOR APPLICATION UNUMBER: US 09/227,421
PRIOR FILING DATE: 1999-01-08
PRIOR FILING DATE: 1999-01-08
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH; 555
TYPE: PRT
CRGANISM: Arabidopsis thaliana
US-09-227-421-2
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US-09-227-421-2
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Best Local Similarity
Matches 314; Conserv
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230 QQISEALVETSVGFETTTMAAAKKKRGQEDVVVVGQKQIVHRKSIDTFGQRTSQYRGVTR
                                                                                                                                                                                                                                                                                                                        118 DFFG----THHNNTSHKEAMDLSLDSLFYNTTH---EPNTTTNFQEFFSFPQTRNH----
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                                                                                                                                                                                                                                                                    158 THPYYSGLACHGLYQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKRINESUNTDDGNUHUWLGFSLSPH-MKM------EATSAATVPTTFYM
                                                 -----GTDSVAVDAKKRGH---AKLGQKQPVHRKSIDTFGQRTSQYRGVTR
                                                                                                     -----GSFNVGV-----YGEFQQSLSLSMSPGSQSSCITGSHHHQQNQNQNHQSQNH 229
                                                                                                                                                            QQMNCGMGNERNGVSLGSVGCGEL~QSLSLSMSPGSQSSCVTAPS--------
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Sequence 2, Application US/09479855

Patent No. 6639128

GENERAL INFORMATION:

APPLICANT: Fischer, Robert L.

APPLICANT: Mizukami, Yukiko

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility

TITLE OF INVENTION: and Enhancing Asexual Reproduction in Plants

FILE REFERENCE: 023070-090720US

CURRENT APPLICATION NUMBER: US/09/479,855

CURRENT FILING DATE: 2000-01-07

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 555

TYPE: PRT
ORGANISM: Arabidopsis thaliana
ORGANISM: Arabidopsis thaliana
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Matches 314; Conserv
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                                                                                                                                                                     G---DNTSNFGVCYGSNPNGGIYSHMSVMPLRSDGSLCLMEALNRSSHSNHHQDSSPKVE
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                                                                                                                                                                                                        SPSQSHLSNFGMCYGVGENGNFHSPLTVMPLKSDGSLCILEALKRSQTQVMVPTSSPKLE
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 QQMNCGMGNERNGVSLGSVGCGEL-QSLSLSMSPGSQSSCVTAPS---
                                                                                                      DFFG----THHNNTSHKEAMDLSLDSLFYNTTH---EPNTTTNFQEFFSFPQTRNH----
                                                                                                                                    DFLGGATMGTHEYGSHERG--LSLDSIYYNSQNAEAQPNRDLLSQPF----RQQGHMSVQ 157
                                                                                                                                                                                                                                         MKSFCDNDDNNHSNTTNLLGFSLSSNMMKMGGRGGREAIYSSSTSSAATSSSSVPPQLVV
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                                                                  THPYYSGLACHGLYQAPLESETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLE 217
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Pred. No. 3.4e-123;
9; Mismatches 113;
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                                                                                                                                                                                                                                                                                                                                            Length 555;
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Sequence 5, Application US/09227421

| Patent No. 655957
| Patent No. 655957
| GENERAL INFORMATION:
| APPLICANT: Fischer, Robert L.
| APPLICANT: Mizukami, Yukiko
| APPLICANT: The Regents of the University of California
| TITLE OF INVENTION: Methods for Altering Organ Mass, Controll:
| TITLE OF INVENTION: and Enhancing Asexual Reproduction in Planting Fill Reference: 023070-090700FC
| FILE REFERENCE: 023070-090700FC
| CURRENT APPLICATION NUMBER: US/09/227,421
| PRIOR APPLICATION NUMBER: US/09/227,421
| PRIOR APPLICATION NUMBER: US/09/227,421
| PRIOR PILING DATE: 1999-01-08
| PRIOR FILING DATE: 1999-01-08
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; ORGANISM: Brassica napus
US-09-227-421-5
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US-09-227-421-5
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SEQ ID NO 5
LENGTH: 548
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                                                                                                                                                                                                                                        Query Match 37.3%;
Best Local Similarity 43.6%;
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110 TMGTHEYG-SHERG--LSLDSIYYNSQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLA 166
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                                                                                                                                         DNDDSNTTNLLGFSLSSNMLKMGGGEALYSSSSSSVATS--SVPPQLVVGDNSSNYGVCY
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                                                             GSNLAAREMYSQMSVMPLRSDGSLCLMEALNRSSHSNNHHHSQV---
                                                                                                 GVG-ENGNFHSPLTVMPLKSDGSLCILEALKRS-----QTQVMVPTSSPKLEDFLGGA 109
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                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                   77;
                                                                                                                                                                                                                   Score 1307; DB 4; Length 548; 
Pred. No. 4.1e-121; 
7; Mismatches 103; Indels 22
                                                                                                                                                                                                                       Indels 220;
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Sequence 5, Application US/09479855
; Patent No. 6639128
; GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mischer, Robert L.
APPLICANT: Mischer, Robert L.
APPLICANT: Mischer, Tukiko
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility
TITLE OF INVENTION: and Enhancing Asexual Reproduction in Plants
FILE REFERENCE: 023070-090720US
CURRENT APPLICATION NUMBER: US/09/479,855
CURRENT APPLICATION NUMBER: US/09/479,855
CURRENT FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
LENGTH: 548
TYPE: PRT
ORGANISM: Brassica napus
OTHER INFORMATION: cannola AINTEGUMENTA (ANT)
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                                                                                                                      NTDDGNNHNWLGFSLSPHM-----KMEATSAATVFTTFYMSPSQ----SHLSNFGMCY
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        GSNLAAREMYSQMSVMPLRSDGSLCLMEALNRSSHSNNHHHSQV----SSPKMEDF----
                                    GVG-ENGNFHSPLTVMPLKSDGSLCILEALKRS------QTQVMVPTSSPKLEDFLGGA 109
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                                                                                 DNDDSNTTNLLGFSLSSNMLKMGGGEALYSSSSSSVATS--SVPPQLVVGDNSSNYGVCY
                                                                                                                                                              Conservative
                                                                                                                                                  37.3%; bu.,
, 43.6%; Pre
                                                                                                                                                          Score 1307; DB 4;
Pred. No. 4.1e-121;
7; Mismatches 103;
                                                                                                                                                                                             Length 548;
                                                                                                                                                            Indels 220;
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US-08-700-152A-4
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COUNTRY; USA

ZIP: 94111-3834

COUNTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION NUMBER: US/08/700,152A
FILING DATE: 20-AUG-1996
CIASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REFERENCE/DOCKET NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-067200US
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08700152A Patent No. 5994622
GENERAL INFORMATION:
APPLICANT: Jochuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: Two Embarcadero Center, E
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                 STREET: Two Embarcae
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                        d and Crew LLP
Eighth Floor
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RESULT 6
US-08-912-272-9
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Best Local Similarity 31.3
Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application Patent No. 6093874
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                            ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
NUMBER OF SEQUENCES: 103
                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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FILING DATE:
                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                            San Francisco
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08912272
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15-AUG-1997
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31.3%; Pred. No. 1.6e-42;
tive 66; Mismatches 150;
                      US/08/912,272
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Best Local S
Matches 69
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,039
FILING DATE: 19-EBB-1998
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Methods for Improving Seeas
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,272
FILING DATE: 15-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jofuku, K
APPLICANT: Okamuro,
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend
STREET: Two Embarca
CITY: San Francisco
                                                                                                                                                                                                                                                                                                     COUNTRY:
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Sequence 9, Application US/09026039 Patent No. 6329567
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 20-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 20-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Region
LOCATION: 44..59
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                           356 GPSTHINFSIENYQVQL 372
                                                                                                                                                                                                                                                                      1 Similarity
69; Conserv
                                                                                                                          GPSTHINFSAENYQKEI 77
                                                                                                                                                                                                 TSOYRGVTRHRWTGRYEAHLWDNSFKKEGHSRKGROVYLGGYDMEEKAARAYDLAALKYW
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ilarity 89.6%;
Conservative
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alpha-helix (SEQ ID NO:37)"
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Pred. No. 1e-30;
3; Mismatches
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US 08/879,827

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LOCATION: 44..59
; OTHER INFORMATION:
; OTHER INFORMATION:
; OTHER OFFER INFORMATION:
US-09-026-039-9
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Best Local Similarity 89.6
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 60950...
Patent No. 60950...
PANERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08912272 Patent No. 6093874
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APPLICATION NUMBER: US 08/
FILING DATE: 20-UN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: PR PC POS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/879,827
FILING DATE: 20-JUN-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS:
                                                                                     APPLICATION NUMBER: FILING DATE: 15-AUG
                                                                                                                                                                                                                                                                                                                                                                                          PLICANT: Okamuro, Jack K.
TLE OF INVENTION: Methods for Improving Seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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alpha-helix (SEQ ID NO:37)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "ANT-R1 direct repeat"
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Pred. No. 1e-30;
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US-09-026-039-10
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GENERAL INFORMATION:
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ZIP: 94111-3834

ZIP: 94111-3834

COMPUTER READABLE FORM:

COMPUTER: FINDY disk

COMPUTER: Flom PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTION DATA:

APPLICATION NUMBER: US/99/026,039

FILING DATE: 19-FEB-198

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 08/912,272

FILING DATE: 15-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912,272

FILING DATE: 15-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912,272

FILING DATE: 15-AUG-1997

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                         ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                         STREET: Two Embarcac
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1..69
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                   COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 ASIYRGVTRHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNF 457
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                                                                                                                                                                                                                                                                                                            California
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Two Embarcadero Center, Eighth Floor
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alpha-helix"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "ANT-R2 direct repeat"
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Pred. No. 6.6e-27;
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                                                                                                                                                                        Version
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APPLICATION NUMBER: US 0 FILING DATE: 20-JUN-1997 PRIOR APPLICATION DATA:

US 08/879,827

US 08/700,152

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US-08-700-152A-1
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPATIBLE: TWOTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jofuku, A. Lander APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: Region NAME/KEY: Region LOCATION: 37.51 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
                        ATTORNEY/ACENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-067200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-067230US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bastian, Kevin REGISTRATION NUMBER:
                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 20-AUG-1996 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide LOCATION: 1..69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398 ASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTPSTQEEAAEAYDVAAIKFRGANAVTNF 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DITRYDVDR 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAAEAYDVAAIKFRGTNAVTNF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08700152A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.9%;
|larity 94.2%;
|Conservative 2
(415) 576-0300
DR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "putative ANT-R2 amphipathic
alpha-helix"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "ANT-R2 direct repeat"
                                                                                                                                                                                    US/08/700,152A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6093874
GENERAL INFORMATION:
APPLICANT: Jofuku
APPLICANT: Okamur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11,
                                                                                            REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/912,272
APPLICATION NUMBER: US/08/912,272
FILING DATE: 15-AUG-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/879,827
FILING DATE: 20-JUM-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/700,152
FILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: ParentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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SITEST: San Franc
CITY: San Franc
California
USA
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TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
Townsend and Townsend
STREET: Two Embarcadero Center, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Domain LOCATION: 1..67 OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
MOLECULE TYPE:
                                                                                                                                                                                                                 NAME: Bastian, Kevin REGISTRATION NUMBER:
                               TYPE: amino
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94111-3834
                TOPOLOGY:
                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 TSQYRGYTRHRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYW 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 67 amino acids amino acid
                                                      amino acid
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                                                                            67 amino acids
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                Linear
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                                                                                                                                                                                                                   34,774
                                                                                                                                                                                                    023070-067220US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d and Crew LLP
Eighth Floor
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RESULT 12
US-09-026-039-11
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Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/879,827
FILING DATE: 20-UUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/700,152
FILING DATE: 20-AUG-1996
ATTORNEY/ACENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: Region
LOCATION: 33..49
OTHER INFORMATION:
OTHER INFORMATION:
                                                                           TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 15-AUG-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                           NAME: Bastian, Kevin L.
REGISTION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION DATA:
PRIOR APPLICATION UNBER: US 08/912,272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..67
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Embarca
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/026,039
                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356
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                                                          amino acid
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Two Embarcadero Center, Eighth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "RAP2.7-R1 direct repeat
                                                                                                                 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Mismatches
                                                                                                                                                                                     023070-067230US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 192.5; DB 3;
Pred. No. 1.3e-11;
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RESULT 13
US-08-700-152A-2
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                                                              US-08-700-152A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application Patent No. 5994622
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Query Match 5.1
Best Local Similarity 60.1
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,152A
FILING DATE: 20-AUG-1996
                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                         FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                       NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jofuku, K
APPLICANT: Okamuro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FITLE OF INVENTION:
                                                                             LOCATION: 1..68
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                           MOLECULE TYPE:
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: I'WO DIMENSION CITY: San Francisco
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                TOPOLOGY:
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               60.3%;
                                                                                                                                                                                                                                                                                                                           576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methods for Improving Seeds
                                                                           /note= "APETALA 2 (AP2) of Arabidopsis direct repeat domain AP2-R2 consisting of amino acids 221-288 of the AP2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "putative RAP2.7-R1 amphipathic
alpha helix (SEQ ID NO:36)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "RAP2.7-R1 direct repeat"
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Score 191.5; DB 2
Pred. No. 1.6e-11;
8; Mismatches 18
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Pred. No. 1.3e-11;
Pred. Mismatches 13;
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                                DB 2;
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                                    68;
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Gaps
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Indels

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US-08-912-272-5
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                                                                                                                                                    US-08-912-272-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Bastian, Kevin L.
REFERENCE/DOCKET NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                Query Match
Query Match
Best Local Similarity 60.3%; Pred. No. 1.6e-11;
Matches 41; Conservative 8; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6093874
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08912272 Patent No. 6093874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0
FILING DATE: 20-JUN-1997
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/879,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0
FILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                  NAME/KEY: Region LOCATION: 33..50 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                        OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 15-AU
                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
398 ASIYRGVTRHQHGRWQARIGRVAGNXDLYLGTESTQBEAAEAYDVAAIXFRGANAVTNF 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            398 ASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEBAABAYDVAAIKFRGANAVTNF 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       California
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                                                                                                                                                                  /note= "putative AP2-R2 amphipathic
alpha-helix (SEQ ID NO:7)"
                                                                                                                                                                                                                                                                        /note= "AP2~R2 direct repeat at
positions 221 to 288"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 08/700,152
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                                                                                                      DB 3; Length 68;
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                                                                                                     Query Match
                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE: 15-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 20-UUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
PILING DATE: 20-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for Improving Seeds
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEB: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 15-AUG-1
                                                                                                                                                           NAME/KEY: Region LOCATION: 33..50 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                LOCATION: 1.68
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two Embarca
CITY: San Francisco
STATE: California
                                                                                 Local Similarity 60.3%;
                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
398 ASIYRGYTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNF 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458 DISRYDVE 465
                                                                41;
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                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (415)
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                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                     5.5%;
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alpha-helix (SEQ ID NO:7)"
                                                                                                                                                                                                                                                                /note= "AP2-R2 direct repeat at positions 221 to 288"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 08/700,152
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                                                            Score 191.5; DB 4; Length 68; Pred. No. 1.6e-11; 8; Mismatches 18; Indels
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                                                              1; Gaps
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Search completed: March 9, 2004, 10:48:10 Job time : 25 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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-FGAPEXT=7 -YGAPOP=10 -YGAPOXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Ygapop 10.0 , 1
Fgapop 6.0 , 1
Delop 6.0 , 1
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3754.413 Million cell updates/sec
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/cgn2 6/ptodata/2/ina/backfiles1.seq:*
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Fgapext
Delext
US-09-227-421-1
US-09-479-855-1
US-09-27-421-4
US-09-479-855-4
US-09-479-855-4
US-08-700-152A-3
US-09-026-039-3
US-09-9313-294A-6727
US-09-198-119C-54
US-09-026-039-1
US-09-026-039-1
US-09-026-039-1
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                   Sequence 1, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 6727, Ap
Sequence 6727, Ap
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
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## ALIGNMENTS

Sequence 1, Application US/09227421
Patent No. 6559357

```
APPLICANT: Mischer, Robert L.
APPLICANT: Mischer, Robert L.
APPLICANT: Mischer, Robert L.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of Interview o
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Oy  238 CysglyGitheuginSerieusernetserieroetyserieusernetserieuser	773 GAAACTAGAAATTACGGGAATGAC			21 pheSerieuSerProHis MetLysMet	h: 2148 rvative: 69 rvative: 69 tches: 116 224 s: 224 -2148) -2148) AspAspGlyAsnAsnHisAsnTrpLeuGly :::
Db 1720	526 ValLeuPheAsnHisProSerGlnGlnGl 1700 546 IleMetAsnCysGlyAsnTyrArgAsnSe ::    1709 GCTCTAAATGCT 566 GlyIleAspSerValGlySerGlyGlnHi	Db 1559 ATTAGGTTCCGTGGCACAAATGCTGTGACTAACTTTGATTTAGGAGGTACGAGGTACGATGTTGAT  Qy 466 ArgIleMetAlaSerSerAsnLeuLeuAlaGlyGluLeuAlaArgArgLysLysAspAsn  Db 1619 CGTATCATGTCTAGTAACACACTCTTGTCTGGAGAGGTAAGGAAGC  Qy 486 AspProArgAsnLysAspIleAspTyrAsnLysSerValValThrSerValAsnAsnAsnGlu  Qy 486 AspProArgAsnLysAspIleAspTyrAsnLysSerValValThrSerValAsnAsnAsnGlu  Db 1670	Db 1379 CATTIGAGAAGGAAGAAGCAGTGCTTTCTCTAGGGGTGCTTCCATCTATAGAGAGAG	Db 1199 AGTAGAAAAGCAAAGCTTTATCTGGGAGGTTATGGAGGAGAAAGCTGCTCGA  Qy 346 AlaTyrAapLeuAlaAlaeLeuLysTyrTTTpGlyProSerThrHisIleAsnbheSerIle  Qy 346 AlaTyrAapLeuAlaAlaeLeuLysTyrTTTpGlyProSerThrHisIleAsnbheSerIle  Db 1259 GCARATGATCTTGCTGCACTCAAGTACTCACCACCAATTTCTCTGCG  Qy 366 GluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArgGlnGluTyrValAla  Qy 366 GluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArgGlnGluTyrValAla  Db 1319 GAGAATTATCAGAAAGAACATGAAGAACACTGACCTAGAAATATGTTTGCA  Db 1319 GAGAATTATCAGAAAGAACATGAAGAACACTGACCTAGAAAAATATGTTTGCA  Db 1319 GAGAATTATCAGAAAGAACATGAAGAACACTGACCTAGAAAAATATGTTTGCA  Db 1319 GAGAATTATCAGAAAAGAACATGAAGAACACTGACCTAGAAAAAAAA	Qy 269 ABBALALYSLYBARGGLYHISALALYSLEUGLYGLNLYSGLNDFOVALHIS Db 1019 GCGAAGAAGAGGGGGACAAGAGGATGTTGTAGTTCAGTCAG
TLEUVAlThrSerLeuSerSerSerArgGluAlaSerGTTGTGGAAGGTGGTTCCAACAAAGAAGTCAGTLeuPheProMetProProMetGluThrLys :::	nGlnAlaAsnGlyAsnGlySerAspGlnLys	ATATCACCAGGTACGATGTAGAT JeuAlaArgArgLysLysAspAsn [  TAGCGCGAAGGAAC ValValThrSerValAsnAsnGlu :::                  NTTGTCGTCAGGAATACT SluAsnAspSerGluTrpLysMet	Schricchicharachachachachachachachachachachachachacha	ATATIGGAGAGAAAGCTGCTC	euGlyGlnLygGlnProValH ::

Oy  1 MetLysArgIleAsmGluSerAsmAsmThrAspAspGlyAsmAsmHisAsmTrpLeuGly Oy  26 ATGAAGTCTTTTTGTGATAATGATAATCATAGCAACAGACTAATTTGTTAGGG 328  Oy  27 PheSerLeuSerProHisMetLysMet	FILE REFERENCE: 023070-090720US CURRENT APPLICATION NUMBER: US/09/479,855 CURRENT FILING DATE: 2000-01-07 NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1 SEQ ID NO 1 LENGTH: 2148 TYPE: DNA CRGANISM: Arabidopsis thaliana PEATURE: OTHER INFORMATION: AINTEGUMENTA (ANT) CDNA NAME/KEY: CDS LOCATION: (269)(1936) COTHER INFORMATION: AINTEGUMENTA (ANT) US-09-479-855-1 Alignment Scores: Pred. No.: 1328.00 Percent Similarity: 3.44e-130 Percent Similarity: 52.84* Best Local Similarity: 52.84* Ouery Match: 37.92* US-09-479-855-1 COMBER OF SEQ ID NOTE: 116 US-09-479-855-1 Alignment Scores: 3.44e-130 Percent Similarity: 43.27* US-09-479-855-1 DB: 1280-00-01-07 US-09-479-855-1 Alignment Scores: 3.44e-130 Percent Similarity: 43.27* US-09-479-855-1 Alignment Scores: 3.4e-130 Percent Similarity: 43.27* US-09-479-855-1 Alignment Scores: 3.4e-130 Percent Scores: 3.4e-130 Percent Scores: 3.4e-130 Per	Qy 624 IleValAsnProlleGlyThrSerValThrSerTrpLeuProSerProThrValGln 642
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APPLICANT: Fischer, Robert L.

APPLICANT: Mizukami, Yukiko

APPLICANT: Mizukami, Yukiko

APPLICANT: Mizukami, Yukiko

APPLICANT: Mizukami, Yukiko

ITILE OF INVENTION: Methods for Altering Organ Mass, Controlling Fert

TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fert

TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fert

TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fert

TITLE OF INVENTION: Methods for Altering Asexual Reproduction in Plants

FILE OF INVENTION NUMBER: US/09/227,421

CURRENT FILING DATE: 1999-01-08

PRIOR APPLICATION NUMBER: US 09/227,421

PRIOR APPLICATION NUMBER: US 09/227,421

PRIOR FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 1738

TYPE: DNA

OCCANATION. Brassica namin
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US-09-227-421-4
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Patent No. 6559357
GENERAL INFORMATION:
ORGANISM: Brassica FEATURE: NAME/KEY: CDS
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| Patent No. 6639128
| GENERAL INPORMATION:
| APPLICANT: Fischer, Robert L.
| APPLICANT: Mizukami, Yukiko
| APPLICANT: The Regents of the University of California
| APPLICANT: The Regents of the University of California
| TITLE OF INVENTION: Methods for Altering Organ Mass, Contro
| TITLE OF INVENTION: and Enhancing Asexual Reproduction in
| FILE REFERENCE: 023070-090720US
| CURRENT APPLICATION NUMBER: US/09/479,855
| CURRENT FILING DATE: 2000-01-07
| NUMBER OF SEQ ID NOS: 8
| SOFTWARE: Patentin Ver: 2.1
| SEO ID NO 4
| LENGTH: 1738
| TYPE: DNA
| ORGANISM: Brassica napus
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Best Local Similarity:
Query Match:
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LOCATION: (1)..(1647)
OTHER INFORMATION: canola AINTEGUMANTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TystysGluGlyGlnThrArgtysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGlu
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                                                                                                                                  TyrargGlyValThrargHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgVal
                                                                                                                                                                                 CAAGAATATGTTGCTCACTTGAGAAGAAAAACCAGTGGTTTCTCTAGGGGTGCTTCCATC
                                                                                                                                                                                                                GlnGluTyrValAlaHisLeuArgArgLysSerSerGlyPheSerArgGlyAlaSerIle
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                                                            TATAGAGGAGTCACCAGACATCACCAGCATGGAAGGTGGCAAGCTCGGATCGGTAGAGTC
TyrAspValAlaAlaIleLysPheArgGlyAlaAsnAlaValThrAsnPheAspIleSer 460
                                    GCTGGAAACAAAGATCTCTACCTTGGAACTTTCGGAACTCAAGAAGAAGCGGCGGAAGCC
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                                                                                                    CCTCAAGTTGGTCCGAAGATGTTCGGAGCAAATGTGGTCGGA---AATATGAGTTCTTGG
                                                                                                                          ProprometGluThrLysIle-----ValAsnProIleGlyThrSerValThrSerTrp
                                                                                                                                                                                LeuSerSerArgGluAlaSerProGluLysArgGlyProSerLeuLeuPheProMet
                                                                           LeuProSerProThrValGlnMetArgProSerProAlaIleSerLeuSerHisLeuPro
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RESULT 5
US-08-700-152A-3
(Sequence 3, Application US/08700152A)
Patent No. 5994622
(Patent No. 1994621
(Patent No. 199462
(Pa

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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COCATION: 190..148;
OTHER INFORMATION:
US-08-700-152A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores: Pred. No.:
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REGISTRATION NUMBER: 34,774
REFERENCE DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                            AspThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgHisArgTrpThrGly 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATGAACTTAACCGGGTCAGACCCAATAACCCACTTGTCACCCATCAGTTCTTCCCCTGAG
                                  AlaAlaLeuLysTyrTrpGlyProSerThrHisIleAsnPheSerIleGluAsnTyrGln
                                                                                                                                                                ArgTyrGluAlaHisLeuTrpAspAsnSerCysLysLysGluGlyGlnThrArgLysGly 329
                                                                                                                                                                                                      CGTGGACCAAGATCAAGAAGTTCTCAGTATAGAGGTGTTACCGTTTTACCGGCGTACCGGA
                                                                                                                                                                                                                                                                                                 AlaLysLysArgGlyHisAlaLysLeuGlyGlnLysGlnProValHisArgLysSerIle 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGATTCTAACGGCGGT----
      AAACAAGTTTACTTAGGTGGATTTGACACTGCTCATGCAGCAGCTCGAGCATATGATAGA
                                                                                           ArgGlnValTyrLeuGlyGlyTyrAspMetGluGluLysAlaAlaArgAlaTyrAspLeu 349
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                                                                                                                                        proGlySerGlnSerSerCysValThrAlaProSerGlyThrAspSerValAlaValAsp
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                                                          Sequence 3, Application Patent No. 6329567 GENERAL INFORMATION:
APPLICANT: Jofuku, K. Diane
APPLICANT: Okamuro, Jack K.
TITLE OF INVENTION: Methods for
NUMBER OF SEQUENCES: 103
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YARRSETGIR   :::   :::   :::   :::   GlnGlnGlyHi   TCAAAATCAAC   LeuTyrGlnAl                                       TAAACGACGA   TCACCAAGTAJ   TCACCAAGTAJ	Alignment Scores:  2.86e-19	; LENGTH: 11721 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic) FEATURE: ; PAME/KEY: - ; LOCATION: 1.11721 ; LOCATION: 1.100RMATION: /note= "Arabidopsis APETALA2 (AP2) OTHER INFORMATION: genomic sequence" US-09-026-039-3	TION NUMBER OF THE PROPERTY OF	ADDRESSEE: Townsend and Crew ILP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA ZIP: 9411-3834 COMPUTER: SEADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/09/026,039 FILING DATE: 19-FEB-1998 CLASSIFICATION LOTA: APPLICATION NUMBER: US 08/912,272 FILING DATE: 15-AUG-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/912,272 FILING DATE: 15-AUG-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/912,272 FILING DATE: 15-AUG-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/912,272 FILING DATE: 20-JUN-1997
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374	1806 TGAGTTGTTATTTATTTATTTTTAAAAATACCGĠAÁGÁÁÁTTTATAAAATTTATTTT 1865  345ArgâlaTyrāspleuālaālaLeulysTyrTrpGlyProSer 358	337	304 9HisArgTrpThrGlyArgTyrGluAlaHisLeuTrp-AspAsn	:::    1226 AGATGGATCGATGAACGTTAACCGGGTCAGACCCAATTAACCCCACTTGTCACCCA 1285 212 SGInGlnValLeuGluGlnGlnMetAsnCysGlyMetGlyAsnGluArgAsnGlyValSe 232

REGISTRATION NUMBER: 34,774 REFERENCE/DOCKET NUMBER: 023070-067230US TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200 TELEPAX: (415) 576-0200 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 11721 base pairs TYPE: mucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE: RAME/KEY: - LOCATION: 1.11721	SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION INJUSE: US/09/026,039 FILING DATE: 19-FEB-1998 CLASSIFICATION INJUSER: US/09/026,039 FILING DATE: 19-FEB-1998 CLASSIFICATION DATA: APPLICATION NUMBER: US 08/912,272 FILING DATE: 15-AUG-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/879,827 FILING DATE: 20-JUN-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/879,827 FILING DATE: 20-JUN-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/700,152 FILING DATE: 20-AUG-1996 ATTORNEY/AGENT INFORMATION: NAME: Bastlan, Kevin L.	RESULT 7  US-09-026-039-3/c  Sequence 3, Application US/09026039  Patent No. 6329567  GENERAL INFORMATION:  APPLICANT: Jofuku, K. Diane APPLICANT: Okamuro, Jack K.  TITLE OF INVENTION: Methods for Improving Seeds  NUMBER OF SEQUENCES: 103  CORRESPONDENCE ADDRESS:  ADDRESSEE: Townsend and Townsend and Crew LLP  STREET: Two Embarcadero Center, Eighth Floor  STATE: California  COUNTRY: USA ZIP: 94111-3834  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: ISM PC compatible  COMPUTER: SYSTEM: DC-DOSCMS-DOS	Qy 423ASHLYBASPLEUTYTLEUGLYTHTTAACTTTGAGTTTTTGTTTG 2282 Qy 423
Qy  319SercyeLysLysGluG 324  Db 10154 CGTTAATCGATCGTACTTTAGATTTAAATTTTATTTTTTTT	Qy 244 uSerLeuSerMetSerProGlySerGlnSerSerCy9ValThrAlaProSerGlyThrAs 264  Db 10351	Qy 169 yLeuTyrGlnAlaProLeuGluGluThrThrLysGluThrHis	; OTHER INFORMATION: /note= "Arabidopsis APETALA2 (AP2) ; OTHER INFORMATION: genomic sequence"  US-09-026-039-3  Alignment Scores:

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US-09-313-294A-6727
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                                                             Sequence 6727, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION;
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGram
SEQ ID NO 6727
LENGTH: 301
TYPE: DNA
FORTHER: 758 TAVE
NAME/KEY: misc_feature
                          ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9676 TGAATTTTATAGATGACTAATTTAACCAAGGAAGAGTTCGTACACGTACTTCGCCGACAA 9617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9439 AATCTTATAAAATAGGTATGTTTATTTGGGTTTGTTCGACACCGAGGTCGAAGCTGCTAG 9380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9499 ATATTCACTCGAAAACTTCATTTTTAGTTTGTTATTTTAACTTTGAGTTTTTGTTTCTTG 9440
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                                                                                                                                                              APPLICANT: Zarka, Daniel
APPLICANT: Jiang, Cai-Zhong
TITLE OF INVENTION. Plant Having Altered Environmental Stress Tolerance
FILE REFERENCE: 19117,713 Seq List
CURRENT APPLICATION NUMBER: US/09/198,119C
CURRENT ELING DATE: 1998-11-23
PRIOR PRIDICATION NUMBER: US 09/018,233
PRIOR APPLICATION NUMBER: US 09/018,233
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/017,816
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,235
PRIOR APPLICATION NUMBER: US 09/018,237
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                                          SOPTWARE: Patentin Ver. 2.
SEQ ID NO 54
LENGTH: 898
TYPE: DNA
ORGANISM: Brassica napus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 54, Application US/09198119C Patent No. 6417428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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  OTHER INFORMATION: bnCBF5 gene
                             FEATURE:
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Gilmour, Sarah
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Conservative:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
RESULT 10
US-09-202-161B-6
; Sequence 6, Application
; Patent No. 6653533
; GENERAL INFORMATION:
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                                                                                                     LysIleMetAsnCysGlyAsnTyrArgAsnSerAlaPhe
                                                                                                                                         GGGATGCTCTTACCGCTGCCGTCCGTACAATGGGGACATAATGATGACTTCGAAGGAGAT
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                                                                                   GCTGACATGAACCTCTGGAATTATTAGTACTCATATTTT
                                                                                                                                                                  --- ValLeuPheAsnHisProSerGlnGlnGlnGlnAlaAsnGlyAsnGlySerAspGln
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158.50
37.00%
22.71%
4.53%
                             US/09202161B
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Mismatches:
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APPLICANT: Purdue Research Foundation
ITILE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
FILE REFERENCE: 7024-371
CURRENT APPLICATION NUMBER: US/09/202,161B
CURRENT FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: CCT/US97/10382
PRIOR FILING DATE: 1997-06-12
PRIOR APPLICATION NUMBER: 60/046,494
PRIOR APPLICATION NUMBER: 60/046,494
PRIOR APPLICATION NUMBER: 60/019,633
PRIOR FILING DATE: 1997-05-14
PRIOR APPLICATION UNMER: 60/019,633
PRIOR FILING DATE: 1996-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: ASCII
SEQ ID NOS: 30
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Best Local Similarity:
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US-09-026-039-1
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Sequence 1, Application US/09026039 Patent No. 6329567
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TYPE: DNA
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                                                                                                                   AsnAsp
                                                                                                                                               ACGGTGACGGTTACGGAAACCGAAACCGAGTCTGTTGCCGACGGTGGAGATAAAAGCGAA
                                                                                                                                                                                  ValThrSerValAsnAsnGluGluThrValGlnValGlnAlaGlyAsnAsnAsnAsnGlu
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Indels:
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GENERAL INFORMATION:
APPLICANT: Jofuku,
APPLICANT: Okamurc
TITLE OF INVENTION:

T: Jofuku, K. Diane T: Okamuro, Jack K. INVENTION: Methods

for

Improving

CWCGIGICIGICATATATACTACATACATACATACATACATACATACATA	191	611 TCACCTGATCACCACGAAGAATCCCGACGGIAGAAIGGGAAAACGGGCIGGAAGAAGGAACGAA	173	AC	rSerGlyLeuAlaCysHisGlyLeuTyrGln	US-10-024-632-2 (1-663) x US-09-026-039-1 (1-1669)	4.416 INCES:	milarity: 32.09% Conservative: Similarity: 21.39% Mismatches: 1.41% Tradels.	3.65e-06 Length: 154.50 Matches:	Scores:	OTHER INFO	; NAME/KEY: misc feature		ION: 11669	; MOLECULE TYPE: DNA (genomic) ; FEATURE:	: sin	; LENGTH: 1669 base pairs ; TYPE: nucleic acid.	; INFORMATION FOR SEQ ID NO: 1: ; SEQUENCE CHARACTERISTICS:	; TELEPHONE: (415) 576-0200 ; TELEFAX: (415) 576-0300	REGISTRATION NUMBER: 34,774 REPERENCE/DOCKET NUMBER: 023070-067230US TELECOMMUNICATION INFORMATION:	ATTORNEY AGENT INFORMATION: NAME: Bastian Revin L.	; PRIOR APPLICATION NUMBER: N: 08/700,152 ; TITING DATE: 20.51G-1896	; APPLICATION NUMBER: US 08/8/9,827; FILING DATE: 20-CM-1997		PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/912,272	866	39	; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOPTWARE: PatentIn Release #1.0, Version #1.30	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	E	STATE: California COUNTRY: USA	Two Embarcadero Center, Eighth Flo	ER OF SEQUENCES: 103 ESPONDENCE ADDRESS: Townsend and Townsen	
RESULT 12	Db 1661 CACT 1664	Qy 404 lThr 405	Db 1601 GCATGTCATTAGAAGGCAAAGCACTGGGTTTCCAAGAGGCAGCTCTAAGTATAGAGGTGT 1660	Qy 384 lAlaHisLeuArgArgLysSerSerGlyPheSerArgGlyAlaSerIleTyrArgGlyVa 404	u	Qy 37738nMetSerArgGlnGluTyrVa 384	1481	371 nLeuGluGluMetLys	Cy 351 discussify into a control of the control of	1361	343AlaAlaArg-AlaTyrAspLeuAlaAl 351		Qy 336342	Db 1241 TATTACTITTTGTTACATATTCAGGTGGATTTGACACAGCACATGCCGCTGCTCGGTATG 1300	Qy 335 335	Db 1181 TTGTGTCCGATTTTTATATGATTTCTTCGACCAAATAAAGGTTTTATTATCTCCTTA 1240	Qy 335 335	Db 1121 GGTATGATCATGTAATGTTGTTCAAACACAGATCAAATATCCTATTGAAACTAAGTTGTG 1180	Qy 335 G1y 335	Qy 317AspasnSerCysLysStysGtuGlyGInTnrArgLysGtyArgGtInValTyrLeG 354	TTACCTATATGGTAAATCTATCAAATACATGTTTCATTTCATTTGAGCCNATACCGTATT			Qy 311 TyrGluAlaHisLeuTrp 316	Db 882 GGTCCTCGCTCACGAGCTCTCAGTATAGAGGAGTTACTTTTTATCGACGAACCGGAAGA 941	Qy 291 ThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgHisArgTrpThrGlyArg 310	Db 828CGTCCGGAAAACCTAGAGCTGGAGATAACACAGCCGGTAAAAAAGAGCCGACGT 881	Qy 271 LysLysArgGlyHisAlaLysLeuGlyGlnLysGlnProValHisArgLysSerIleAsp 290	Db 786 AGAAACCAGTCTCTTGTTCGGTCGAATCCTAGCGGGTCTGGT 827	Qy 251 GlySerGlnSerSerCysValThrAlaProSerGlyThrAspSerValAlaValAspAla 270		231	Qy 211 ThrHisGlnGlnValleuGluGLnGlnWetAsnCysGlyMetGlyAsnGluArgAsnGly 230  21 TCGAATCAAATCATGGAACAG752	ייייייייייייייייייייייייייייייייייייי

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TITLE OF INVENTION. Plant Having Altered Environmental Stress Tolerance;
FILE REFERENCE: 19117.713 Seq List
COURRENT APPLICATION NUMBER: US/09/198,119C
CURRENT FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: US 08/706,270
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: US 09/018,233
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,233
PRIOR APPLICATION NUMBER: US 09/017,816.
PRIOR APPLICATION NUMBER: US 09/018,235
PRIOR APPLICATION NUMBER: US 09/018,235
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,235
PRIOR APPLICATION NUMBER: US 09/017,575
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; Sequence 86, Application US/09198119C
; Patent No. 6417428
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Best Local Similarity:
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; FEATURE:
; OTHER INFORMATION: brCBF7 gene
US-09-198-119C-86
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SEQ ID NO 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-02-03
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495 AsnLysSerValValThrSerValAsnAsnGluGlu---
                                                                                                                                                                                          464 ValGluArgIleMetAla----------SerSerAsnLeuLeu 474
                                                                                                                                                                                                                                          407 TCGGCTTGGCCGCTCCGTATCCCGGAGACAACCTGCGCCAAGGATATCCAGAAGGCTGCT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 ValAlaGlyAsnLysAspLeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGlu 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                400 | | IleTyrArgGlyValThrArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArg 419
                                            GGCATGAACATGGCTTCTCAGGTTGAGGTTAATGACACGACGGATCATGACCTGGACATG 586
                                                                                         AlaGlyGluLeuAlaArgArgLysLysAspAspAspProArgAsnLysAspIleAspTyr 494
                                                                                                                                              GCTGAAGCCGCATTGGCTTTTGAGGCGGAGAAGAGTGATACCACGACGACGAATGATCAT 526
                                                                                                                                                                                                                                                                                                                                         AlaTyrAspValAlaAlaIleLysPheArgGlyAlaAsnAlaValThrAsnPhe----- 457
                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAAACAAGAAATCTAGGATTTGGCTCGGAACTTTCAAAACAGCTGAGATCGCAGCTCGT 346
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Jiang, Cai-Zhong
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MESSUIT 13
US-09-198-119C-70
Sequence 70, Application US/09198119C
Patent No. 6417428
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Best Local Similarity:
                                                                                                                                 US-10-024-632-2 (1-663) x US-09-198-119C-70 (1-950)
                                                                                                                                                                                               Query Match:
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SEQ ID NO 70
LENGTH: 950
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APPLICANT: Jiang, Cai-Zhong
APPLICANT: Jiang, Cai-Zhong
TITLE OF INVENTION: plant Having Altered Environmental Stress Tolerance
FILE REFERENCE: 19117.713 Seq List
CURRENT FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: US 08/706,270
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: US 08/706,233
PRIOR APPLICATION NUMBER: US 09/018,233
PRIOR APPLICATION NUMBER: US 09/017,816
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,235
PRIOR APPLICATION NUMBER: US 09/018,235
PRIOR APPLICATION NUMBER: US 09/018,235
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APPLICANT: Stockinger,
APPLICANT: Jaglo-Ottos
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PRIOR APPLICATION NUMBER: US 09/017,575
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,227
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
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NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Brassica oleracea FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
420 ValAlaGlyAsnLysAspLeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGlu 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  528 PheAsnHisProSerGlnGlnGlnGlnAlaAsnGlyAsnGlySerAspGlnLysIleMet 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 507 -----ThrValGlnValGlnAlaGlyAsnAsnAsnAsnGluAsn 519
                                           261 ÁTTTÁCCGÁGGÁGTT---CGCCTTAGAAAATCAGGTAAGTGGGTGTGAAGTGAGGGAA 317
                                                                                 400 [leTyrArgGlyValThrArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          767 TTACCGCCGCCGTCCGTACAATGGGGACATAATGATGACTTCGAAGGAGATGCTGACATG
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Jaglo-Ottosen, Kirsten
Gilmour, Sarah
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Matches:
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APPLICANT: Zarka, Daniel
APPLICANT: Jiang, Cai-Zhong
ITILE OF INVENTION, Plant Having Altered Environmental Stress Tolerance
FILE REFERENCE: 1911,713 Seq List
CURRENT APPLICATION NUMBER: US/09/198,119C
CURRENT FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: US 09/018,233
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,233
PRIOR APPLICATION NUMBER: US 09/018,23
PRIOR APPLICATION NUMBER: US 09/018,23
PRIOR APPLICATION NUMBER: US 09/017,816
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,235
PRIOR APPLICATION NUMBER: US 09/018,235
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/017,575
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,227
PRIOR APPLICATION NUMBER: US 09/018,227
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,227
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PRIOR FILING DATE: 1998-02-03
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SEQ ID NO 52
LENGTH: 874
TYPE: DNA
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5. 6417428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGCCGCCGTCCGTACAATGGGGACATAATGATGACTTCGAAGGAGATGCTGACATGAAC 857
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                                                                                     PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomashow, Michael
Stockinger, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jaglo-Ottosen, Kirsten
Gilmour, Sarah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------ThrValGlnValGlnAlaGlyAsnAsnAsnGluAsnAsp 520
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                                                                                                     Sequence 21, Application US/09533029
Patent No. 6664446
GENERAL INFORMATION:
APPLICANT: Heard, Jacqueline
APPLICANT: Broun, Pierre
APPLICANT: Broun, Pierre
APPLICANT: Keddie, James
APPLICANT: Rieddie, James
APPLICANT: Pineda, Omaira
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                           US-09-533-029-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 GlyGluLeuAlaArgArgLysLysAspAspAspProArgAsnLysAspIleAspTyrAsn 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 TCGGCTTGGCGGCTCCGTATCCCGGAGACAACCTGCGCCAAGGATATCCAGAAGGCTGCT 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            754 CCGCCGCCGTCCGTACAATGGGGACATAATGATGACTTCGAAGGAGATGTTGACATGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                529 AsnHisProSerGlnGlnGlnGlnAlaAsnGlyAsnGlySerAspGlnLysIleMetAsn 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       694 GAGGAGTGGATGTTCGGGATGCCGACCTTGTTGGCTGATATGGCGGCAGGGATGCTCTTA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     634 GAGACGACGGTGGAGGGTGTTGTTCCGGAGGAACAGATGAGCAAAGGGTTTTACATGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274 CCAAACAAAAATCTAGGATTTGGCTCGGAACTTTCAAAACAGCTGAGATCGCAGCTCGT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400 IleTyrArgGlyValThrArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArg 419
Samaha, Raymond
Zhang, James
Yu, Guo-Liang
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                                                                                     Adam, Luc
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147.00
37.80%
25.36%
4.20%
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APPLICANT: Ratcliffe, Oliver
APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Reuber, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-010
CURRENT APPLICATION UMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
FEARLIER FILING DATE: 199-03-23
INUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.1
SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: G19 US-09-533-029-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Arabidopsis thaliana FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                    301 GTTTATAGAGGGATA----CGTAAGCGTCCATGGGGAAAATGGGCCGGCTGAGATTCGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                     400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 ArgGlnGluTyrValAlaHisLeuArgArgLysSerSerGlyPheSerArgGlyAlaSer 399
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AAGGGCCGTAAACTC-------ACGGCTGAGGAACTCTGGTCAGAGCTCGAT 165
                       AspSerGluTrpLysMetValLeuPheAsnHisProSerGlnGlnGlnGlnAlaAsnGly 539
                                                                                                                                                           ArgArqLysLysAspAsnAspProArgAsnLysAspIleAspTyrAsnLysSerValVal 499
                                                                                                                                                                                                                            SerArgTyrAspValGluArgIleMetAlaSerSerAsnLeuLeuAlaGlyGluLeuAla 479
                                                                                                                                                                                                                                                                                       AlaTyrAspValAlaAlaIleLysPheArgGlyAlaAsnAlaValThrAsnPheAspIle 459
                                                                                                                                                                                                                                                                                                                                IleTyrArgGlyValThrArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArg 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCGTTGTC-----TCTCAGAGT
                                                                                                                                                                                               CTGCACCATCCT------CCTCCTCCTAATTATACTCCTCCGCCGTCATCG 522
                                                                                             ThrSerValAsnAsnGluGluThrValGlnValGlnAlaGlyAsnAsnAsnAsnGluAsn 519
                                                                                                                               CCACGATCAACCGATCAGCCTCCGGCGAAGAAG----
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                                                                      682 AAACAGCAGATATCGAGCTTGGAATCGTTCCTTGAGCTGGACGGTAACACGGCGGAGCAA
 742 CCGAGTCAGCTTGATGAGTCC 762
                           HisAsnMetLeuAspGluSer 581
                                                                                                       SerAlaPheSerMetAlaLeuGlnAspLeuIleGlyIleAspSerValGlySerGlyGln 574
                                                                                                                                            TTTGGAAATGGGGACGAGTTTCAGAACCTGAGTTACGGATTTGAGCCGGATTATGATCTG 681
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Search completed: March 13, 2004, 08:01:55 Job time : 131 secs

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Run
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-MODEL-frame+ p2n.model -DEV=xlh
-MODEL-frame+ p2n.model -DEV=xlh
-Q=/Ggn2_1/USPTO_Spool/US10024632/runat_09032004_101207_10754/app_query.fasta_1.839
-DB=N Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-DB=N Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-DOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MAXT=100.0THR SUNGS=0 -THR MAX=100 -THR MIN=0 -ALIGN=15
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -QUTFMT=pto -NOEM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10024632 @CGN 1 1 352 @runat 09032004 101207 10754 -NCFU=6 -ICFU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEDUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEDUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                       1408.5
1349.5
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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Match
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1: geneseqn1980s:*
2: geneseqn1990s:*
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3502
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100.0
49.0
40.2
38.5
37.9
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                   ABN84480
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                   Abn84480 Soybean A
Abn84481 Soybean A
Abn84482 Soybean A
Abn84484 Rice AINT
Abn84484 Rice AINT
Aac43005 Arabidops
Aaa59200 CDNA enco
Abx13437 A. thalia
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## ALIGNMENTS

ARSSULT 18
ARSSALT 18 Glycine max. Soybean AINTEGUMENTA-like polypeptide GmANT1 cDNA ABN84480; ABN84480 standard; cDNA; 2344 BP He SS, 21-DEC-2000; 2000US-0257896P. 19-DEC-2001; 2001WO-US049294 01-AUG-2002. WO200259332-A2. plant; gene; ss. AINTEGUMENTA; ANT-like polypeptide; GmANT1; soybean; transgenic plant; 21-OCT-2002 (first entry) (MONS ) MONSANTO TECHNOLOGY LLC. Dotson SB Location/Qualifiers 242. .2233 /product= "GmANT1" /\*tag=

cDNA enco

WPI; 2002-599798/64. P-PSDB; ABB79636.

New nucleic acids encoding AINTEGUMENTA-like polypeptides useful in improving agronomic, horticultural, and quality traits of plants, such as increased size of plant organs.

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Example 1; Page 127-130; 169pp; English.

The present sequence is that of cDNA encoding GmANT1, a newly identified CC AINTEGUMENTA-like (ANT-like) polypeptide of soybean. The cDNA comprises CC the insert of clone CPR67663, which was obtained from a soybean sequence Cd database screening using Arabidopsis ANT as query. Also isolated was CC clone CPR67666 (see ABN94481) encoding GmANT2 (see ABN9637). GmANT1 and CC GmANT2 show homology to ANT in 2 N-terminal Ap2 DNA binding domains, but CC chave ction provides nucleic acids encoding ANT-like polypeptides CC comprising, in the N-terminal to C-terminal direction, 2 Ap2 DNA binding CC comprising, in the N-terminal to C-terminal direction, 2 Ap2 DNA binding CC comprising, in the N-terminal to C-terminal direction, 2 Ap2 DNA binding CC conding the ANT-like polypeptides across selected from those given in ABB79629-35. ANT-like polypeptides have been identified in soybean, CC rice, cotton and corn (see ABB79638-41). Nucleic acids (see ABN94480-86) CC encoding the ANT-like polypeptides can be used in the construction of transgenic plants, especially corn, soybean, canola, wheat, cotton, cc tother quality traits, such as increased size of plant organs. These CC plants are especially useful for production of ethanol or animal CC encoding the such as increased size of plant organs. These CC encoding the such as increased size of plant organs. These condulate expression of endogenous ANT-like gene expression, in sense co-suppression to modulate expression of endogenous ANT-like gene spression, in sense co-suppression to material plant production of the plant organs are technology to condulate expression of endogenous spread and plant due to a mutation in one or more endogenous genes encoding the ANT-like polypeptides

XX more endogenous genes encoding the ANT-like polypeptides

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Sequence 2344 BP; 738 A; 472 C; 548 G; 586 T; 0 U; 0 Other;

Db 602	Qy 121	Db 542	Cy 101	Db 482	0у 81	Db 422	Qy 61	Db . 362	Qy 41	Db 302	Qy 21	Db 242	4 29	US-10-024-632-2	Percent Simila Best Local Sim Query Match: DB:	Alignment Scor Pred. No.: Score:
102 AGAGGTTTGAGCCTAGACAGCATCTATTATAACTCCCAAAAACGCAGAGGCTCAACCCAAC 661	.21 ArgGlyLeuSerLeuAspSerIleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsn 140	42 AAATTGGAGGACTTTCTAGGTGGTGCAACTATGGGAACTCACGAATATGGAAGCCACGAG 601	.01 LysLeuGluAspPheLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGlu 120	82 TGTATCTTGGAAGCTCTCAAAAGATCACAAACGCAAGTGATGGTGCCAACTTCGTCTCCG 541	81 CYSIIeLeuGluAlaLeuLYSArgSerGlnThrGlnValMetValDroThrSerSerPro 100	22 GAAAATGGTAACTTCCATTCTCCACTTACGGTTATGCCTCTCAAGTCTGATGGGTCACTT 481	61 GluAsnGlyAsnPheHisSerProLeuThrValMetProJeuLysSerAspGlySerLeu 80	62 TICTACATGTCCCCTTCTCAATCTCACTTGTCCAACTTCGGAATGTGTTACGGTGTCGGA 421	41 PheTyrMetSerProSerGlnSerHisLeuSerAsnPheGlyMetCysTyrGlyValGly 60	02 TROTOTOTOTOACCOCACATGAAAATGGAGGCTACTTCAGCAGCCACTGTTCCGACAACC 361	21 PheSerLeuSerProHisMetLysMetGluAlaThrSerAlaAlaThrValProThrThr 40	42 ATGAAGCGCATAAAATGAGAGTAACAACACCGATGATGGAAACAATCATAACTGGTTGGGG 301	1 MetLygArgIleAsnGluSerAsnAsnThrAspAspGlyAsnAsnHisAsnTrpLeuGly 20	32-2 (1-663) x ABNB4480 (1-2344)	Similarity: 100.00% Conservative: 0 al Similarity: 100.00% Mismatches: 0 tch: 100.00% Indels: 0 tch: 6 Gaps: 0	3.96e-284 Length: 3502.00 Matches:

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1682 CGTAAGAAAGATAACGATCCTAGAAACAAGGACATAGACTACAACAAGAGTGTAGTAACA 1741

	rqAspLeuLeuSerGlnProPheArgGlnGlnGlyHisMetSerValGlnThrHisPr
	62 AGAGACCTTCTTCACAACCCTTC
	161 TYrTyrSerGlyLeuAlaCysHisGlyLeuTyrGlTAAlaProLeuGluGluGluThrThr 180 
	1 LysGluThrHisValSerAspCys
	201 AsnTrpValAlaProThrArgGluPheSerThrHisGlnGlnValLeuGluGlnGlnMet 220 
	221 AsnCysGlyMetGlyAsnGluArgAsnGlyValSerLeuGlySerValGlyCysGlyGlu 240
	241 LeuGInSerLeuSerLeuSerMetSerProGlySerGInSerSerCysValThrAlaPro 260
	261 SerGlyThrAspSerValAlaValAspAlaLysLysArgGlyHisAlaLysLeuGlyGln 280
	281 LysGlnProValHisArgLysSerIleAspThrPheGlyGlnArgThrSerGlnTyrArg 300 
	301 GlyValThrargHisArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCys 320 
	321 LyslysgluglyglnthrarglysglyargglnValTyrLeuGlyglyTyrAspMetGlu 340 
	341 GluLysAlaAlaArgAlaTyrAspLeuAlaAlaLeuLysTyrTrpGlyProSerThrHis 360 
	361 IleasnPheGerIleGluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArg 380 
	381 GlnGluTyrValAlaHisLeuArgArgLysSerSerGlyPheSerArgGlyAlaSerIle 400 
•	401 TYRATGGIYVƏLTHTARGHISHISGINHISGIRYATGTTPGIRALƏARGILEGIYATGVƏL 420 
	421 AlaGlyAsnLysAspLeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGluAla 440 
	441 TYRASDVALALAALAILELYSPheArgGlyAlaAsnAlaValThrAsnPheAspIleSer 460 
	461 ArgTyrAspValGluArgIleMetAlaSerSerAsnLeuLeuAlaGlyGluLeuAlaArg 480 
	481 ArgLysLysAspAsnAspProArgAsnLysAspIleAspTyrAsnLysSerValValThr 500

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RESULT 2
ABN84481
ID 8488
XX ABN8
XX ASN
AC ABN8
XX AINT
KW Plan
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KW Plan
XX Glyc
FH Key
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                                                                                                                                                                                                                                                                                                                                                       19-DEC-2001; 2001WO-US049294.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AINTEGUMENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABN84481
New nucleic acids encoding AINTEGUMENTA-like polypeptides useful in improving agronomic, horticultural, and quality traits of plants, such
                                                                                       WPI; 2002-599798/64.
P-PSDB; ABB79637.
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                                                                                                                                                                                                                                       MONSANTO TECHNOLOGY LLC
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                                                                                                                                                                                  SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 25. .2022
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/product= "GmANT2"
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> Example 1; Page 134-137; 169pp; English increased size of plant

The present sequence is that of cDNA encoding GmANT2, a newly identified AINTEGUMENTA-like (ANT-like) polypeptide of soybean. The cDNA comprises CC the insert of clone CPR67626, which was obtained from a soybean sequence Cd database screening using Arabidopsis ANT as query. Also isolated was CC clone CPR67663 (see ABN94480) encoding GmANT1 (see ABN97636). GmANT1 and CC GmANT2 show homology to ANT in 2 N-terminal AP2 DNA binding domains, but have C-terminal sequences that bear little, if any, homology to ANT. The CC invention provides nucleic acids encoding ANT-like polypeptides (comprising, in the N-terminal to C-terminal direction, 2 AP2 DNA binding domains followed by an amino acid subsequence selected from those given comprising, in the N-terminal to C-terminal direction, 2 AP2 DNA binding domains followed by an amino acid subsequence selected from those given comprising conton and corn (see ABB79636-41). Nucleic acids (see ABN9480-86) (comprise followed by an amino acid subsequence selected from those given conton and corn (see ABB79636-41). Nucleic acids (see ABN9480-86) (comprise followed by an amino acid subsequence selected from those given conton plants, especially corn, soybean, cannola, wheat, cotton, comprise for plants, especially corn, soybean, cannola, wheat, cotton, corn for the construction of the construction of plants are especially useful for production of plant organs. These corporates endogenous ANT-like gene expression, in sense co-suppression to modulate expression of endogenous ANT-like gene sapression, in sense co-suppression to markers for traits linked to those genes that they are part of, as genetically and physically mapping the genes that they are part of, as compression of endogenous ANT-like genes, or in the identification of compression of endogenous and the plant of a mutation in one or more endogenous genes encoding the ANT-like polypeptides

Sequence 2323 BP; 746 A; 482 C; 492 G; 603 T; 0 U; 0 Other;

Ś Š 밁 Ś Query Match: DB: Percent Similarity: Best Local Similarity: 밁 밁 US-10-024-632-2 (1-663) x ABN84481 (1-2323) Мо.: 145 GCTGCTGAAGTGGTTCCTACAAGCTTTTACCACCACACTGCTCCA------CTTAGTAGC S 85 25 SerAlaAlaThrValProThrThrPheTyrMetSerProSerGlnSerHisLeuSerAsn ;;:||| MetLysArgIleAsnGluSerAsnAsnThrAspAspGlyAsnAsnHisAsnTrpLeuGly TTCTCACTCTCTCTCAAATGCATAATATAGGAGTTTCTTCACACTCACAACCTTCCTCT 5.51e-134 1715.00 65.86% 54.00% 48.97% Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 2323 378 83 165 74

84

20

144 32

52

198

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91 258

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72 MetProLeuLysSerAspGlySerLeuCysIleLeuGluAlaLeuLysArgSerGlnThr

TATGGTTTCTACTATGGACTTGAAGCTGAAAATGTTGGATTGTATTCAGCTTTGCCAATC PheGlyMetCysTyrGlyVal---GlyGluAsnGlyAsnPheHisSerProLeuThrVal

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259

92

S

128 IleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArgAspLeuLeuSerGlnPro

147

127 378

438

495

GlyThr---HisGluTyr------GlySerHisGluArgGlyLeuSerLeuAspSer CAAGCAATGGCTACTTCAACACCAAAACTGGAGAACTTCTTAGGTGGGGAAGCCATG GlnValMetValProThrSerSerProLysLeuGluAspPheLeuGlyGlyAlaThrMet ATGCCCCTCAAATCTGATGGCTCTCTCTATGGAAACTTTTAAGCAGGTCACAAGCA 318

GGGACCCCTCATCACTÁCGAATGTAGTGCCACAGAAACAATGCCTCTGÁGCTTÁGÁCÁGT

GTTTTTÄĊ---ATCCAACCCTCACGCCGTGACCCAAATAATAACCAAACCTACCAAAAC

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                                              ValGluArgIleMetAlaSerSerAsmLeuLeuAlaGlyGluLeuAlaArgArgLysLys
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New nucleic acids encoding AINTEGUMENTA-like polypeptides useful
                                                        WPI; 2002-599798/64
P-PSDB; ABB79638.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNAB, suggesting tissue-specific expression. Initial OsaNTI clones had CC been identified in a rice database screening using the newly identified Sybpen ANT-like polypeptide GmaNTI as query. An additional rice clone (see ABN84483) encoding OsaNT2 (see ABB79639) was also isolated OsaNT1 CD polypeptide shares high homology with Arabidopsis ANT, GmaNT1 and GmANT2 CC at the N-terminal AP2 DNA binding domains, shares conserved segments at CC not with ANT, at the C-terminus. The invention provides nucleic acids encoding ANT-like polypeptides comprising, in the N-terminal to C-C terminal direction, 2 AP2 DNA binding domains followed by an amino acid consumption and corn (see CC polypeptides were identified in soybean, rice, cotton and corn (see CC polypeptides were identified in soybean, rice, cotton and corn (see CC polypeptides can be used in the construction of transgenic plants, CC especially corn, soybean, canola, wheat, cotton, tomato or potato (all craimed) having improved agronomic, horticultural or other quality craits, such as increased size of plant organs. These plants are CC enabled having also be used in antisense technology to suppress CC endogenous ANT-like gene expression, in sense co-suppression to modulate expression of endogenous ANT-like genes, as probes for genetically and physically mapping the genes that they are part of, as markers for traits of linked to those genes, or in the identification of loss of function cutant phenotypes of a plant due to a mutation in one or more endogenous construction in one or more endogenous construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the coding region for OSANT1, a newly identified AINTEGUMENTA-like (ANT-like) polypeptide of rice. The CDNA was obtained by PCR amplification using gene-specific primers (see ABN84496-97) using paniale cDNA as template. The cDNA was not amplified from root or leaf cDNAs, suggesting tissue-specific expression. Initial OSANT1 clones had
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgGlyAlaAsnAlaValThrAsnPheAspIleSerArgTyrAspValGluArgIleMet
                                                                                                                                                                                                                                                                                                                                                    ---GCTCATCTCCCTGTTTTTGCAGCCTGGACAGAT 1923
                                                                                                                                                                                                                                                                                                                                                                               LeuSerHisLeuProValPheAlaSerTrpThrAsp 662
                                                                                                                                                                                                                                                                                                                                                                                                                                     TrpLeuProSerProThrValGln------MetArgProSerProAlaIleSer 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ĠCTCTCCACGGCATTGTCGGGTTCGACGTCGAGTCGGCGGCAGCTGACGAGATCGAT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyAsnGlySerAspGlnLysIleMetAsnCysGlyAsnTyrArgAsnSerAlaPheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TrpLysMetValLeuPheAsnHisProSerGlnGlnGlnGlnAla------Asn 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGGACCATGTGCCAATAGGCCGCGAGCTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaSerSerAsnLeuLeuAlaGlyGluLeuAlaArgArgLysLys---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuSerSerSerArgGluAlaSerProGluLysArgGlyProSerLeuLeuPheProMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspGluSerSerLysIle --- GlyThrHisPheSerAsnThrSerSerLeuValThrSer 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---AspAsnAspProArgAsnLysAspIleAspTyrAsnLysSerValValThrSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTGGCCTGAACGCGGTGACGAACTTTGACATCACAAGGTACGACGTGGACAAGATCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCCCGGGAAGGATCAGTGGCATCAACTTCTCGAACTCGTCTTCGCTGGTGACTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AsnAsnGluGluThrValGlnValGlnAlaGlyAsnAsnAsnAsnGluAsnAspSerGlu 522
                                                                                                                                                                                                                                                                                                                                                                                                           TGGATGCCGATGCCGGCCGGCCGCAGCTCACGTGATGAGGCCGCCGAGTGCCATT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProProMetGluThrLysIleValAsnProIleGlyThrSerValThrSer-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAGCAACTCGAGGGGGGGGGGGCCCTGAGAGGCCTTGGCCTCGCCATGCTCTACGCCAAG 179
                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                ANT-like polypeptide; OsANT1; rice; transgenic
                                                                                                          Location/Qualifiers
                                                                    'product= "OsANT2
                                                                                  *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----CATCCCACCGCCGTCAGCCTCGCCGCCATGAACCCC 183:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATGGATCACAGCAGCAAGCTGCAGCGTGCACCGAA 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GGTGCG 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1443
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              6
                                                                                                                                                                                                                                                                                                                                                                                              Alignment
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2010 BP;
                                                                                                                                                                                                                                                                                                                                                                                              No.:
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The present sequence is the coding region of the rice OsANT2 gene cancoding a newly identified AINTEGUMENTA-like (ANT-like) polypeptide. The COSANT2 gene (see also AEN84483) was isolated following a rice database screening using soybean ANT-like polypeptide GRANT1 as query. Another rice clone (see AEN84482) encoding OsANT1 (see AEN79638) was also comprising, in the N-terminal to C-terminal aNT-like polypeptide success and the color of the polypeptide of the color of the rection, 2 AP2 polypeptides comprising, in the N-terminal to C-terminal direction, 2 AP2 polypeptides comprising, in the N-terminal to C-terminal direction, 2 AP2 polypeptides were identified in soybean, rice, cotton and corn (see AEB7963641). Nucleic acids (see CC AEN84480-86) encoding the ANT-like polypeptides were identified in the construction of transgenic plants, especially corn, soybean, canola, wheat, cotton, tomato or potato (all claimed) having improved agronomic, cotton, tomato or potato (all claimed) having improved agronomic, cotton, tomato or potato (all claimed) having improved agronomic, corgans. These plants are especially useful for production of ethanol or cryans. These plants are especially useful for production of ethanol or suppression to modulate expression of endogenous ANT-like gene expression, in sense copupression to modulate expression of endogenous ANT-like genes, as probes for markers for traits linked to those genes, or in the color in one or more endogenous genes encoding the ANT-like to a color polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acids encoding AINTEGUMENTA-like polypeptides useful improving agronomic, horticultural, and quality traits of plants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-599798/64.
P-PSDB; ABB79639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-2001; 2001WO-US049294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 151-154; 169pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 improving agronomic, horticultu
increased size of plant organs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-DEC-2000; 2000US-0257896P.
                                            polypeptides
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<u>ن</u>
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344 A; 681

Db	γ	Db	γQ	DЪ	Qy	<b>d</b> d	Q Y	В	Ş	US-10-024	DB:	Query Match:	Best Local Similarity:	Percent Similarity:	Score:	Pred. No.:
285	67	225	57	171	48	112	3 2	55	13	-632		ch:	1 51	imil		. 8
CGGGTTCTC			rGlyValGlyGluAsn		rHig					-2 (1-663)		,	milarity:	arity:		
TCCATGCCGCT	rValMetProLe	CATGACGCCGT	GluAsn	resectettet	;	JACGATGTCGGC	-ThrSerAlaAl	GCGGCTGGCTC	disasnTrpLeu	US-10-024-632-2 (1-663) x ABN84484 (1-2010)	σ	38.54%	48.02%	57.32%	1349.50	2.3e-103
CAAGTCCGACGGCTCGCT	uLysSerAspGlySerLe	rcgrcaccrccgcggccgc		GCATGGAGGTGGGCTGTTCTACAACCCTGCCGCCGTCGCCTCCTTC		CACCACCACCACCAC	laThrValProThrThrPh	GGATTCTCGCTGTCGCC	:GlyPheSerLeuSerPro	(1-2010)	Gaps:	Indels:	Mismatches:	Conservative:	Matches:	Length:
CGGGTTCTCCATGCCGCTCAAGTCCGACGGCTCGCTCTGCATCATGGAGGCACTCCG 344	luAlaLeuLy	CGGCGGCGGCATGACGCCGTCGTCACCTCCGCGGCCGGCGGCGGATCGTACTATGGCGC 284	SeSe	TACTA	LeuSerAsnPheGlyMetCysTy 57	GGCGGCGTCGACGATGTCGGCCACCACCACCACCACGTGCACCAGCAT-CAGCAGCA 170	-ThrSerAlaAlaThrValProThrThrPheTyrMetSerProSerGlnSe	GEAGGTGTCGGCGGCTGGGATTCTCGCTGTCGCCGCACATGGCGACGTACTGCGCC	GlyAsnAsnHisAsnTrpLeuGlyPheSerLeuSerProHisMet-LysMetGluAla 31	••	35	161	153	9	351	2010
344	87	284	67	224	57	170	<b>4</b>	111	31							

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1055 GGGCGTATGATCTTGCTGCGCTCAAGTACTGGGGCCCTTCCACGCACATCAACTTCCCGT 1114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 lnThrargLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGluGluLysAlaAlaA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435 CCTGGACACTCCGCCTTCTACGACGGCGGCGACGGTCACCAC------477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 rleuasp-----SerIleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArgAs 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405 hrarqHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgValAlaGlyAsnLysA 425
                                                                                                                                          385 laHisLeuArgArgLysSerSerGlyPheSerArgGlyAlaSerIleTyrArgGlyValT 405
                                                                                                                                                                                                                                                                      365 leGluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArgGlnGluTyrValA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 875 ACCGCAAGTCCATTGACACGTTCGGCCAGAGGACGTCGCAGTACAGAGGCGTCACCAGGC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 alAspAla-----LysLysArgGlyHisAla---LysLeuGlyGlnLysGlnProValH 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      755 GETECEÁGTÉCAGETGÉGTÉACETGEAGGECGÉCGCCGCGGÉGAGCCGTACATGGÉCA 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 lyserGlnSerSerCysValThr------AlaProSerGlyThrAspSerValAlaV 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  695 GCCCCATCATCCCCACCGGCGGCCACCTGCACCCTCTCACCCTGTCCATGAGCTCGGCCG 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 ------SerProg 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           643 -----GGCGGCGGCTACGACATCGCCAACGCCGCCGACGACGTC---TGCGCCCCCG 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 snCysGlyMetGlyAsnGluArgAsnGlyValSerLeuGlySerValGlyCys----- 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 snTrpValAlaProThrArgGluPheSerThrHisGlnGlnValLeuGluGlnGlnMetA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGluGlyLeuLysA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 yrserGlyLeuAlaCysHisGlyLeuTyrGln---AlaProLeuGluGluGluThrThrL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           478 -----CAGGGACACGCCCAGGACGCGGCGGCGTCGGTGGCGACCGCGCACCACGG 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 8-----ArgSerGlnThrGlnValMetValProThrSerSerProLysLeuGluAspPh 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCysLysLysGluGlyG 325
                                                                                                           CTCACCTCAGAAGGAAAAGCAGTGGCTTCTCGCGTGGCGCTTCGATCTACCGTGGAGTCA 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                         AGACCAGAAAAGGACGCCAAGTGTATCTTGGTGGGTATGACATGGAGGAGAAGGCTGCCA 105
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                                                                                                                     protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                  Arabidopsis thaliana DNA fragment SEQ ID NO: 37674.
                                                                                                                                                                                                                                                         17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                              AAC43005;
                                                                                                                                                                                                                                                                                                                                                               AAC43005 standard; DNA; 1668 BP
                                     Arabidopsis thaliana
                                                                                      promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1475 GCACGCTCCTCCCGGGGGAGCTGGCGCGGCGCGCAAGGGTAAGGTCGGCGACGGCGGCGGCGC- 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1415 TCHACGCCGTCACCTACTTCGACATCACGAGGTACGACGTGGACAAGATCCTGGAGAGGA 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1976 ACCTGCCAATGTTCGCCGCGTGGACCGAC 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1756 -- GCGCCGCACATGTCGATGGCGGCG-----ACGAGCCTGGGCAACTCCCGGGAGC 1804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1672 -----CTGCATGACCTCCTGCCGACGCCTCTCGGTG---CTGCAGGACATCG 1720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1613 CGCTGCCAGCGGCGAGAACGGAGCAGCAGCAGCATGGGCACGGCGCCACCAA- 1671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1568 TOCAGGCCGGG------AACGTGGCGGAGTGGAAGATGGCCACCGCCGCCG 1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1355 CCGGCACGCAGGAGGAGGCGGCGAGGCGTACGACGTGGCGGCGATCAAGTTCCGGGGGGC 1414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1805 AGÁGCCTGAC---ÁGGGGGGTCGGCGGCGGCGGCGGCGGCGTCCTCGCCACGCTGT 1861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1862 TCGCCAAGCCCGCGGCGCGTCGAAGCTGTACAGCCCGGTG-----CCGCTGAACACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          604 laSerProGluLysArgGlyPro-----------SerLeuLeuP 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          528 -----PheAsnHisProSerGlnGlnGlnGlnAlaAsnGlyAsnGlySerAspGlnL 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  490 ysAspIleAspTyrAsnLysSerValValThrSerValAsnAsnGluGluThrValGlnV 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          432 --SerThrGlnGluGluAlaAlaGluAlaTyrAspValAlaAlaIleLysPheArgGlyA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         635 rpleu---ProSerProThrValGlnMetArgProSerProAla---IleSerLeuSerH 653
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64 AsnPheHisSerProLeuThrValMetProLeuLysSerAspGlySerLeuCysIleLeu E ::::	30GluAlaThrSerAlaAlaThrValProThrThrPheTyrMet 4 121 TCATCTTCTACCTTCTAGCTGCAACTTCTTCTTCTTCTTGTTCCACCTCAACTTGTTGTT  44 SerProSerGlnSerHisLeuSerAspheGlyMetCysTyrGlyValGlyGluAsnGly 6 181 GGTGACAACATAGCAACTTTGGTGTTTGCTATGGATCTAACCCAAATGGA 2	Qy 1 MetlysArglleAsnGluSerAsnAsnThrAspAspGlyAsnAsnHisAsnTrpLeuGly 20 Qy 1 MetlysArglleAsnGluSerAsnAsnThrAspAspGlyAsnAsnHisAsnTrpLeuGly 20	ignment Scores:  ed. No.:  1.13e-101  More:  1328.00  Morent Similarity:  52.84%  St Local Similarity:  43.27%  Morent Annual An	26-OCT-1999; 990 26-OCT-1999; 991 26-OCT-1999; 991 28-OCT-1999; 990 28-OCT-1999; 991 28-OCT-1999; 991	21-OCT-1999; 99U 21-OCT-1999; 99U 22-OCT-1999; 99U 22-OCT-1999; 99U 22-OCT-1999; 99U 25-OCT-1999; 99U 25-OCT-1999; 99U	14-0CT-1999; 99U 14-0CT-1999; 99U 14-0CT-1999; 99U 18-0CT-1999; 99U 21-0CT-1999; 99U 21-0CT-1999; 99U 21-0CT-1999; 99U	PR 23-SEP-1999; 99US-0155486P.  PR 24-SEP-1999; 99US-0156559P.  PR 28-SEP-1999; 99US-0156458P.  PR 29-SEP-1999; 99US-015656P.  PR 04-OCT-1999; 99US-0157753P.  PR 05-OCT-1999; 99US-0157753P.  PR 07-OCT-1999; 99US-0158029P.  PR 07-OCT-1999; 99US-0158029P.  PR 13-OCT-1999; 99US-0158369P.  PR 13-OCT-1999; 99US-0159233P.  PR 13-OCT-1999; 99US-0159233P.  PR 13-OCT-1999; 99US-0159233P.  PR 14-OCT-1999; 99US-0159234P.  PR 14-OCT-1999; 99US-0159339P.
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                                                                                                                                                                                                          Aintegumenta; ANT; cell proliferation; growth; organ mass; fertility; asexual reproduction; plant; male sterile plant; female sterile plant
                                                                                                                                                                                                                                                                            cDNA encoding an Arabidopsis aintegumenta (ANT) polypeptide.
                                                                                                                                                                                                                                                                                                                          07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                    AAA59220;
                                                                                                                                                                                                                                                                                                                                                                                                             AAA59220 standard; cDNA;
    WO200040694-A2
                                                                                                                                                   Arabidopsis sp
                                                                                                                                                                                            asexual reproduce early flowering;
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                                                                                  Location/Qualifiers 269. .1936
                                                                /*tag=
                                           'product= "aintegumenta polypeptide"
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Best Local Similarity:
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           문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes an aintegumenta (ANT) polypeptide. The ANT gene is expressed and functions not only in developing ovules but also it various developing organs. Growth and cell proliferation in plant can be modulated by modulating ANT activity. Modulation of ANT activity is used to alter organ mass, control fertility and enhance assexual reproduction in plants. Increased ANT activity can be used to produce male or female sterile pilants. Inhibition of ANT activity can be used to truncate vegetative growth, resulting in early flowering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modulating growth and cell proliferation in a plant used to alter organ mass, control fertility and enhance asexual reproduction in plants comprises modulating ANT activity and selecting plants with altered cell
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             GATCTTAGCTTAGATAGTTTATTCTACAACACCACTCAT--
                                                ---LeuSerLeuAspSerIleTyrTyrAspSerGlnAsnAlaGluAlaGlnProAspArg
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                                                                                                                                                                                GAAGCTCTCAACAGATCTTCTCACTCGAATCACCATCAAGATTCATCTCCAAAGGTGGAG
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IleLysDheArgGlyAlaAsnAlaValThrAsnPheAspIleSerArgTyrAspValGlu 465
                                                                                                                        CATTTCAGAAGGAAGAGCAGTGGTTTCTCTAGGGGGTGCTTCCATCTATAGAGGAGTCACA
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                                                                                                    MetArgProSerProAlaIleSerLeuSerHisLeuProValPheAlaSerTrpThrAsp
                                                                                                                                     ileVal---AsnProIleGlyThrSerValThrSerTrpLeuProSerProThrValGln
                                                                                                                                                                                                            ACTCCCGAGAGACTCTTGAGTTTTCCGGCGATTTTCGCGTTGCCTCAAGTTAATCAAAAG
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                                 Thr 663
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ABX13437 standard; DNA; 2148

04-JUN-2003

(first entry)

A. thaliana AINTEGUMENTA DNA corresponding to Genbank U40256

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Expression cassette; transgenic; promoter; LOX5; plant; food production; animal feed; seed; stress resistance; disease resistance; starch content lipid content; dormancy; fibre content; pharmaceutical production; sterile plant; vitamin; flavouring; perfume; dye; cotyledon; embryonic tissue; stress factor; LOX; ds. 11-JUN-2001; 12-DEC-2002. Arabidopsis thaliana. 2001DE-01027882

11-JUN-2001;

(BADI ) BASF

PLANT SCI 2001DE-01027882

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-GAGCCCAACACG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel cassette for the transgenic expression of nucleic acid containing the promoter of the LOX5 gene from Arabidopsis CC thaliana or deletion variants of the LOX5 promoter which are functionally liked to the mucleic acid of the invention. The cassette is used to compare transgenic organisms, especially plants, for production of foods, animal feeds, seeds (including those with increased resistance to stress cc and disease, altered starch/lipid contents or dormancy, or altered fibre content), pharmacceuticals (especially antibodies, vaccines, enzymes and cc pharmaceutical proteins) and fine chemicals (especially enzymes and contents), pharmacceuticals (especially antibodies, vaccines, enzymes and contents), pharmacceuticals (especially antibodies, vaccines, enzymes and cc perfumes and dyes), also to produce sterile plants. The LOX5 promoter cc provides strong and specific expression in cotyledons and/or other early cm provide strong and specific expression in cotyledons and/or other early cc embryonic tissues are particularly sensitive. Since cotyledons are the cm storage organs of seeds, expressing transgenes in them produces crayledons is homogeneous, there are no side effects on other plant corgans (pollen) and the promoter is functional value. Expression in the corgans (pollen) and the promoter is functional value. Expression in the corgans (pollen) and the promoter is functional value variety of cc plants (ornamentals or crops). This sequence associated with the Arabidopsis thaliana LOX gene described in the disclosure of the invention
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TCATCTTCAACTTCTGCAGCTGCAACTTCTTCTTCTTCTGTTCAACTTGTTGTTGTT
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                                                                                                                                                                  GluAlaLeuLysArgSerGlnThrGlnValMetValProThrSerSerProLysLeuGlu 103
                                                                                                                                                                                                                                                                                                         SerProSerGlnSerHisLeuSerAsnPheGlyMetCysTyrGlyValGlyGluAsnGly
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---LeuSerLeuAspSerIleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArg 141
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                                                            GATTTCTTTGGG-
                                                                                          AspPheLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGluArgGly---
                                                                                                                                    GAAGCTCTCAACAGATCTTCTCACTCGAATCACCATCAAGATTCATCTCCAAAGGTGGAG
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                                IleLysPheArgGlyAlaAsnAlaValThrAsnPheAspIleSerArgTyrAspValGlu 465
                                                                                                  LeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGluAlaTyrAspValAlaAla
                                                                                                                                                                                        ArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgValAlaGlyAsnLysAsp 425
                                                                                                                                                                                                                                  CATTTGAGAAGGAAGAGCAGTGGTTTCTCTAGGGGTGCTTCCATCTATAGAGGAGTCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes an aintegumenta (ANT) polypeptide. The ANT gene is expressed and functions not only in developing ovules but also in various developing organs. Growth and cell proliferation in plant can be modulated by modulating ANT activity. Modulation of ANT activity is used to alter organ mass, control fertility and enhance asexual reproduction in plants. Increased ANT activity can be used to produce male or female sterile plants. Inhibition of ANT activity can be used to truncate vegetative growth, resulting in early flowering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulating growth and cell proliferation in a plant used to mass, control fertility and enhance asexual reproduction in comprises modulating ANT activity and selecting plants with
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Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering phenotypes in plants such as sunflower, coconut, soybean, wheat and
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P-PSDB; ABR40856.
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The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a polypeptide (PP) having receptor-like protein kinase activity, mitogen activated protein (MAP)-kinase activity, LIP15-like transcription factor
                                                                                                                                                                                                                                                                   Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering phenotypes in plants such as sunflower, coconut, soybean, wheat and phenotypes in plants such as sunflower, coconut, soybean, wheat and provided the such as sunflower, coconut, soybean, wheat and provided the such as sunflower, coconut, soybean, wheat and provided the such as sunflower, coconut, soybean, wheat and provided the such as suc
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ira IC, Sakai H, Shen
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AGTAGCATCATGAA-CTCTCACTTAACTCAAGGAATCATTAACAACTATGCAGCAGGAGG 1665
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  AACAACAGCGACTCATCATCATAACTGGCACAATGCTCTTGCATTCCACCAACCTCAACC 1725
                                                                                                                  AsnAsnAsnGluAsnAspSer-GluTrpLysMetValLeuPheAsnHisProSerGlnGl
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                                        nGlnGlnAlaAsnGlyAsnGlySerAspGlnLysIleMetAsnCysGlyAsnTyrArg--
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P-PSDB; ABR40766.
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Sakai H, Shen I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a compressing a nucleic acid sequence (NS) chosen from a NS encoding a copyopetide (PP) having receptor-like protein kinase activity, mitogen activated protein (MAP)-kinase activity, LIP15-like transcription factor activity and CKC-like transcription factor activity. Also described: (1) cc activity and CKC-like transcription factor activity. Also described: (1) cc complement (II) of (I); (2) a chimeric construct (III) comprising (I) or comprising (III) in its genome; (4) seeds (y) obtained from (IV); and (5) cc comprising (III) in its genome; (4) seeds (y) obtained from (IV); and (5) coll obtained from (V). (I) or its part can be used in antisense conjunction or co-suppression in a transformed plant. (III) is useful for canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for creating transgenic plants having altered lipid profiles. (I) can also be used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
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                                   IleAspTyrAsnLysSerValValThrSer------
                                                                                                                                                            ArgTyrAspValGluArgIleMetAlaSerSerAsnLeuLeuAlaGlyGluLeuAlaArg
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                                                                   CGTTTGAAGGATATGGAGCAGGTTGAACTGAGTGTGGATAATGGTCATAGAGCAGATCAA
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Kinney
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> y Ы, Cahoon Klein JR, Epelbaum S, Famodu Li C, Oliveira IC, CO, Harvell Sakai H, Si B

Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering oil phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.

Claim 18; Page 379-380; 542pp; English.

CC The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a CC polypeptide (PP) having receptor-like protein kinase activity, mitogen activated protein (AMP)-kinase activity, LIPIS-like transcription factor activity and CKC-like transcription factor activity. Also described: (I) cc complement (II) of (I); (2) a chimeric construct (III) comprising (I) or CC (II), operably linked to a regulatory sequence; (3) a plant (IV) and (5) cc comprising (III) in its genome; (4) seeds (V) betained from (IV); and (5) cc inhibition or co-suppression in a transformed plant. (III) is useful for canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for creating transgenic plants having altered lipid profiles. (I) can also be used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to canola, present sequences used in the exemplification of the present construction.

414 A; 231 Ç 321 ٠<u>.</u> 324 ., 0 U; 0 Other;

4.05e-76 1022.00 63.39% 52.63% 29.18% Length:
Matches:
Conservative:
Mismatches:
Indels: 1290 230 47 90 71

US-10-024-632-2 (1-663) x ACC00805 (1-1290)

ThrAspSerValAlaValAspAlaLysLysArgGlyHisAlaLysLeuGlyGlnLysGln GluGlyGlnThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGluGluLys ThrargHisargTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCysLys ProValHisArgLysSerIleAspThrPheGlyGlnArgThrSerGlnTyrArgGlyVal TyrValAlaHisLeuArgArgLysSerSerGlyPheSerArgGlyAlaSerIleTyrArg PheSerIleGluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArgGlnGlu AlaAlaArgAlaTyrAspLeuAlaAlaLeuLysTyrTrpGlyProSerThrHisIleAsn CCAGTTCCTCGCAAATCTATTGACACTTTTGGGCAAAGAACATCTCAATATCGTGGTGTT GTT---CAAGTGAATGAGGATAGTAGGAAAACGGGTCATGGCGAAATCTCATGCTAGAGAA SerLeuSerLeuSerMetSerProGlySerGlnSerSerCysValThrAlaProSerGly GCAGCAAAGGCTTACGACTTAGCTGCACTCAAGTATTGGGGTCCAACAACTCACATAAAT GAAGGGCAAACAAGGAAAGGAAGGCAAGTTTACCTTGGTGGTTATGATAAGGAAGAAAAA **ACAAGGCATAGATGGACTGGAAGATATGAGGCCCATTTGTGGGATAATAGTTGCAGAAAG** AGTTTGTCCCTCACTATGAGCCCCAGTGTGCAAAATGGG---GTGGGTGCAATTTCCTCT 322 402 119 419 382 359 362 299 342 302 62 179 239

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RESULT 13 ABN84483 ID ABN84483; XX ABN84483; XX  DT 21-OCT-2002 (first entry) XX XX DE Rice AINTEGUMENTA-like polypeptide OBANT2 gene. XX XX XX AINTEGUMENTA; ANT-like polypeptide; OBANT1; rice; transgenic plant; XX XX XX VPlant; gene; ds. XX XX Oryza sativa.	618 -ProProMetGluThrLys1leValAsnPro1leGlyThrSerValThrSerTrpLeuPr 637	558 SerMetAlaLeuGlnAspLeuIleGlyIleAspSerValGlySerGlyGlnHisAsnMet 577  890	483 LysAspAsnAspProArgAsnLysAspIleAspTyrAsnLysSerVal 498 720 CCTAAAGAATCACCAGCTCCGGTTCCTGCCTCTGACTTCAATTCGTGCGGTTCATCGCCG 779 499 ValThrSerValAsnAsnGluGluThrValGlnValGlnAlaGlyAsnAsnAsnAsnGlu 518 ::::::::::::::::::::::::::::::::::::	### 10 TITGTCGCCAATTTAAGAAGGAAGAAGAGTGGATTTTCAAAGAGGGCATCTGTGTATAGA 479  #### 403 GlyValThrArgHisHisGlpHisGlyArgTrpGlnAlaArgIleGlyArgValAlaGly 422  #### 403 GlyValThrArgHisHisGlpHisGlyArgTrpGlnAlaArgIleGlyArgValAlaGly 422  #### 403 GlyValThrArgHisHisGlpHisGlyArgTrpGlnAlaArgIleGlyArgValAlaGly 422  #### 403 GlyValThrArgHisHisGlpHisGlyArgTrpGlnAlaArgIleGlyArgValAlaGlyArgValAlaGlyArgTrpGlyGlyArgTrpGlnGluGluAlaArgArgTTGCAGGA 539  ##### 403 GlyValThrArgHisHisGlyThrPheSerThrGlnGluGluAlaAlaGluAlaTyrAsp 442  #### 423 AsnLysAspLeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGluAlaTyrAsp 442  #### 424 AACAAGGACTTGTATCTTGGTACAACTTTAGCACAAGAAGAAGCACTATGAT 599  ##################################
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3792 TCTCTGCAACTGCACTATGATCTAGTAGTTATTCTTGTCCGGATTCTTCTCATCATG 3851 432	1 3 1 0-2 4 1 7 1 4 -4 2 2 3 7 7 7 7	2053 GCTGATGAAATGTATGTATGTATGTTCTTGCATGATCATCCTGCTGAATCTTTTGGCATGGG 3012
613 euLeuPheProMetBroProMetGluThrLysileValAmprolleGlyThrSerValT  613 euLeuPheProMetBroProMetGluThrLysileValAmprolleGlyThrSerValT  614839 CGCTGTTCGCCAAGCCCGCGGCGGCGTCGAAGCCTGTACAGCCCGGTGCCGCTGA  625 hrSerTrpLeuProSerProThrValGlnMetArgProSerProAlaIleSerL  626 i::	0y   432	

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Alignment
Pred. No.:
Score:
                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                   The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a CC polypeptide (PP) having receptor-like protein kinase activity, mitogen CC activity, caleosin-like activity, LTP15-like transcription factor cc contivity and CKC-like transcription factor activity. Also described: (1) CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or CC (II), operably linked to a regulatory sequence; (3) a plant (IV) and (5) CC comprising (III) in its genome; (4) seeds (V) obtained from (IV), and (5) CC contivity and from (V). (I) or its part can be used in antisense (CC contile the oil phenotype in a transformed plant. (III) is useful for CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for CC creating transgenic plants having altered lipid profiles. (I) can also be used as a hybridisation probe. ACC00626 to ACC00668 and ARA40591 to invention
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                                                                       US-10-024-632-2 (1-663) x ACC00799 (1-1874)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase; receptor-like protein kinase; mitogen activated protein kinase; oil; LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1; CKC-like transcription factor; antisense inhibition; co-suppression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering oil phenotypes in plants such as sunflower, coconut, soybean, wheat and rice
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Jones TJ,
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P-PSDB; ABR40764.
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                                                                                                                                                                                                     Sequence 1874 BP;
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                         184 AACTGGCTTTCGTTCTCTCTCTCCCCA---ATGGAAATGCTCCGAACCTCCGAACCTCAG
 37 ValProThrThrPheTyrMetSerProSerGlnSerHisLeuSerAsnPheGlyMetCys 56
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PIONEER HI-BRED INT INC.
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Kinney AJ,
i MC;
                                               AsnTrpLeuGlyPheSerLeuSerProHisMetLysMetGluAlaThrSerAlaAlaThr 36
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49.84%
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27.20%
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Klein TM,
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Indels:
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SerPro 30 SerPro 68 AGTGAC 36 AGTGAC 36 LysArg 88 LysArg 88 LysArg 88 LysArg 88 CTTTCG 38 GGGAC 44 SerIle 12 ATCTAC 55 TACTTC 55 TACTTC 55 TALLys 18 AACTCC 66 LysAsn 26 LysAsn 26 LysAsn 27 AGULeu	382 GluTyrValAlaHisLeuArgArgLys	362 AsnPheSerIleGluAsnTyrGlnValGlnLeuGluGluMe	342 LysalaalaargalaTyraspLeualaalaLeuLysTyrT: 	322 LysGluGlyGlnThrArgLysGlyArgGlnValTyrLeuGlyG :::	302 ValThrArgHisArgTrpThrGlyArgTyrGluAlaHisLev 	282 GlnProValHisArg_ysSerIleAspThrPheGlyGlnArg] :::	62 GlyThrAspSerValAlaValAspAlaLysLysArgGlyHis ::: 93 AATAGCTCG	42 GlnSerLeuSerLeuSerMetSerProGlySerGlnSerSer	22 CysGlyMetGlyAsnGluArgAsnGlyValSerLeuGlyS	02 TrpValAlaProThrArgGluPheSerThrHisGl	82 GluThrHisValSerAspCysSerSerLeuMetProGlnMet	69 GlyLeuTyrGlnAlaProLeuGluGlu	49 ArgGlnGlnGlyHisMetSerValGlnThrHisProTyrT	9 TyrTyrAsmSerGlnAsnAlaGluAlaGlnProAsnArgAs     ::: 7 CGTTACTCCGACAGCCAGACGGAGACGCAGGACTCGTCG	AlaThrMetGlyThrHisGluTyrGlySerHis ::::: TCCTCCGCC	89 SerGlnThrGlnValMetValP       ::: 82 TCGCAGAGCGTCGGCCACGTGC	9 LeuThrValMetProLeuLysSerAspGlySerLeuCysIleL ::::: 1 GTGAGTTTTGTTGAA	TyrGlyVa1GlyGluAsnGlyAsn 	41 TICCTICAATACGACGCCGCTTCCGCTACTICCTCAC
	—н	tLysAsnMetSerArgGln     ::::::::::     aaaCaTGTAACAAAGCAA	rpGlyProSerThrHisIle         ::: GGGGTCCCACTGCTACCACC	GlyTyrAspMetGluGlu          ggatatgataaggaagaa	euTrpAspAsnSerCysLys              artgggaCAATAGTTGCAGA	rgThrSerGlnTyrArgGly           GACTTCTATTTACAGAGGT	sAlaLysLeuGlyGlnLys	rCysValThrAlaProSer 26	erValGlyCysGlyGluLeu 24 ::     CAACCGGA73	lnGlnMetAsn 22	ThrGluGlyLeuLysAsn	rThrLys	SerGlyLeuAlaCysHis 1 ::: GGTTCTACTTCGTACTTC 5	pLeuLeuSerGlnProPhe 1 	erLeuAspSerIle 1 ::: GTGATG 4	GlyGly 1	euGluAlaLeuLysArg 88	rPro 6	

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RESULT 15
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ID ADD30
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                                                                                                                                  ds; transcription factor seed germination rate;
                                                                                                                                                                       Plant yield-related polynucleotide clone G1793.
                                                                                                                                                                                                15-JAN-2004
                                                                                                                                                                                                                       ADD30878;
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09-AUG-2001; 2001US-0310847P-
19-NOV-2001; 2001US-0336049P-
                                                                                                           Arabidopsis thaliana
                                    09-AUG-2002; 2002WO-US025805
                                                            20-FEB-2003
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                                                                                                                                                                                                                                                                                                                       oMetProPro
                                                                                                                                                                                                (first entry)
                                                                                                                                    factor; transgenic plant; ;
rate; plant vigor; seedling
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                                                                                                                                       growth rate;
g vigor.
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Ratcliffe O,
Pilgrim ML,
Broun PE;
                                                        The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polynucleotides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant such as an alteration in a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and flower senescence. Sequence information related to the polynucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New plant transcription factor polynuclectides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate
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14-JUN-2002; 2002US-00171468.
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Sequence 1818
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Jiang C, Reuber TL, Creelman RA, Pineda C,
        BP;
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Query Match: No.: 5.52e-70 951.50 48.61% 36.90% 27.17% Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 1818 252 80 157 194 23

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467 1108	448 PheArgGlyAlaAsnAlaValThrAsnPheAspIleSerArgTyrAspValGluArgIle
447 1048	428 LeuGlyThrPheSerThrGlnGluGluAlaAlaGluAlaTyrAspValAlaAlaIleLys 
427 988	408 HisGlnHisGlyArgTrpGlnAlaArgIleGlyArgValAlaGlyAsnLysAspLeuTyr 
407 928	388 ArgarglysserSerGlyPhoSerArgGlyAlaSerIleTyrArgGlyValThrArgHis 
387 868	368 TyrGinValGinLeuGluGluMetLysAsnMetSerArgGinGluTyrValAlaHisLeu 
367 808	348 ASPLeuAlaAlaLeuLySTyrTrpGlyProSerThrHisIleAsnPheSerIleGluAsn 
347 748	328 IYBG1YATGG1NValTYrLeuG1YG1YTYrAspMetG1UG1ULYSAlaAlaArgAlaTYr 
327 688	308 ThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCysLysLysGluGlyGlnThrArg
307 628	288 SerīleAspThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgHisArgTrp
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267 514	SGlySerGlnSerSerCysValThrAlaProSerGlyThrAspSerValAla 
247 454	228 ArgAsnGlyValSerLeuGlySerValGlyCysGlyGluLeuGlnSerLeuSerLeuSer :
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### TYPASHLYBSerVal

Search completed: March 13, 2004, 05:51:51 Job time : 486 secs

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Listing first 45 summaries
        GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Sequence 1 from Patent WO02059332.
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Nicotiana tabacum
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2546 bp mRNA
Nicotiana tabacum ANT-like protein mRNA,
AY461432
AY461432.1 GI:38492171
                                                                                                                                                                 2 (bases 1 to 2546)
Rieu, I. and Mariani, T.
Direct Submission
Submitted (07-NOV-2003) Plant Cell Biology, University of Nijmegen,
Toernooiveld 1, Nijmegen 6525 ED, The Netherlands
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               Spermatophyta, Magnoliophyta, asterias; lamiids; Solanales; (bases t to 2546)
Rieu, I. and Mariani, T.
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                                         /organism="Nicotiana tabacum"
/mol type="mRNA"
/culfivar="petit havana SR1"
/db xref="taxon:4097"
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  note="similar to Arabidopsis thaliana/codon_start=1
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GluGlyLeuLysAsnTrpValAlaProThrArgGluPheSerThrHisGlnGlnValLeu | | | | | | | | ::: | | | | :::
                                                                                                                                          ThrHisProTyrTyrSerGlyLeuAlaCysHisGlyLeuTyrGlnAlaProLeuGluGlu 177
                                                                                              GluThrThrLysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThr---
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NPFILDDQQNKIGNHFSNASSLVTSLGSSREASFDKSAASLVFAKPTNVNACIPSAQL
RPIPVSISHLPVFAALNDA"
                                                             - À CAAAA CCAA CT CAAATTT CA CATT GTGATGCCCAAAT GACTGCAGTGTCTGGA
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Gaps:
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REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

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DEFINITION ACCESSION VERSION

SOURCE ORGANISM

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                                                                                                                                                                                                                                                                           LysAspIleAspTyrAsnLysSerValValThrSerValAsnAsnGluGluThrValGln 509
                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGTAAATGCTGTCACAAACTTTGACATATCGCGATACGACGTGGAGAAAATCATGGCT
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GGAAATTATAGAAACCCAACTTTTTCCATGGCATTACAAGATCTAATCGGTATTGATTTG
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                                                                                                                          HisProSerGlnGlnGlnAlaAsnGlyAsnGlySerAspGlnLysIleMetAsnCys 549
                                                                                                                                                                   AATGACAACAACAATGGGAATAATGTCACAGATTGGAAAATGGTGTCATAT---
                                                                                                                                                                                              ValGlnAlaGlyAsnAsnAsnAsnGluAsnAspSerGluTrpLysMetValLeuPheAsn
                                                                                                                                                                                                                                                                                                                                      SerSerAsnLeuLeuAlaGlyGluLeuAlaArgArgLysLysAspAsnAspProArgAsn 489
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                  Percent Similarity:
Best Local Similarity:
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Nucleic acid molecules associated wit growth and uses thereof Patent: WO 02059332-A 3 01-AUG-2002; Monsanto Technology LLC (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycine max (soybean)
Glycine max
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots;
Tosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AX555218
Sequence 3 1
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                                                                                                                                                                                                       /Godon_start=1
//proteIn_id="CAD58226.1"
//proteIn_id="CAD58226.1"
//db_xref="G1:2898747"
//db_xref="G1:2898747"
//db_xref="G1:2898747"
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SWEVANPQASHAHESKMIVPHYEENAGESGSIGSMAYGDLQSLSLSMSPSSQSSVTS
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AHLWDNSCKKEGQSRKGRGVVLGGYDMEEKAACAYDLAKLKYWGPSTHINFPLENYQN
ELEBMUNMTRQEYVAHLRRKSSGFSRGAMYRGVTRHHQHGRWQARIGRVGANKDLYL
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NETQCLDQNHRKFSAYEDTQEAILMHQKSCESENDQWKWVLYQSSQQDLEQNPFTIESD
RTNQSFAVALDNMFHQEVESESKAFTHYSNBSSATSLSSSREGSPDRTSLPMLSGMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="unassigned
/db_xref="taxon:3847"
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                                                           ValhibargLysSerIleAspThrPheGlyGlnArgThrSerGlnTyrArgGlyValThr 303
                                                                                                                                                                                                                                                                                                                                HisGlnGln------ValLeuGluGlnGlnMetAsnCysGlyMetGlyAsnGluArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerAlaAlaThrValProThrThrPheTyrMetSerProSerGlnSerHisLeuSerAsn
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                   ArgHisArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCysLysLysGlu 323
                                                                                                                   GATTCTGTTGCCATGGATACTAAGAAAAGGGGGGCCTGAAAAGGTTGACCAGAAGCAAATT
                                                                                                                                             AspSerValAlaValAspAlaLysLysArgGlyHisAlaLysLeuGlyGlnLysGlnPro
                                                                                                                                                                                                   SerProGlySerGlnSerSerCysValThr------AlaProSerGlyThr
                                                                                                                                                                                                                                                              AsnGlyValSerLeuGlySerValGlyCysGlyGluLeuGlnSerLeuSerLeuSerMet 248
                                                                                                                                                                                                                                                                                                     CATGAGTCAAAGATGATTGTTCCTCATGTGGAGGAAAATGCTGGTGAATCAGGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                       AGCCAAACTTCTGACAACAACCATCTTCATGTTCAAAACATGGGTGGTGATGATGCCGTT
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Sequence 5
                                                                                            MetArgProSerProAlaIleSerLeuSerHisLeuProValPheAlaSerTrpThrAsp 662
                                                                                                                                                                                                                                                        AspGlnLysIleMetAsnCysGlyAsnTyrArgAsnSerAlaPheSerMetAlaLeuGln
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                                                                                                                                     AAACTATTGGCTACTAATCCAAATAACGTGAATTCTTGGGACCCCTTCACCCCATTTGAGG
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Nucleic acid molecules associated with
growth and uses thereof
Patent: WO 02059332-A 5 01-AUG-2002;
Monsanto Technology LLC (US)
Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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HQLVPYNYQPLTEAEMLQEAAAAPMEDAMAAAKNELVTSYSQGQDAEDASRAAQH
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VHRKSIDTFGQRTSQYRGVTRHWTGRYEAHLMDNSKNGGGTRAGROYYLGGYDTED
KAARAYDLAALKYWGLSTHINFFLENYADEIEEMERMTRQEYVAHLRRSSGFSRGAS
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DITRYDVDKIMESSSLLPGEAARKVKAIEAAPDHVPIGRELGATEEASAADEIDVPGGXISG
INFSNSSSLVTSLSNSREGSPERLGLAMLYAKHHPTAVSLAAVNPWKFMPAPAAAHVM
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/db_xref="GI:25898749"
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/mol_type="unassigned DNA"
/db_xref="taxon:4530"
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      FLI_CDNA; oligo capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Cryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa (japonica cultivar-group)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GCTCTCCACGGCATTGTCGGGTTCGACGTCGAGTCGGCGGCAGCTGACGAGATCGAT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyAsnGlySerAspGlnLysIleMetAsnCysGlyAsnTyrArgAsnSerAlaPheSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---AspAsnAspProArgAsnLysAspIleAspTyrAsnLysSerValValThrSerVal 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CETEGECTGAACGCGGTGACGAACTTTGACATCACAAGGTACGACGTGGACAAGATCATG 1383
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                                                                                                                                                                                                                                                                                                                                                                                          LeuSerHisLeuProValPheAlaSerTrpThrAsp 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TrpLeuProSerProThrValGln------MetArgProSerProAlaileSer 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAT---
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                                                                                                                                                                                                                                                                                                                                                                                                                            TGGATGCCGATGCCGGCGCCGGCCGCAGCTCACGTGATGAGGCCGCCGAGTGCCATT---
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Suzuki,Y.,
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                                                                                                                                                          Embryophyta; Tracheophyta; la; Poales; Poaceae;
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A clone:002-101-C10, full
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RS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Adachi, J., Aizawa, K., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hedd, R., Hiramoto, K., Hiraoka, T., Hayashida, K., Hayashizaki, Y., Ishida, Y., Ishedd, R., Imamura, K., Immotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kibuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Knodo, S., Konno, H., Kouda, M., Kodama, T., Kojima, Y., Knodo, S., Konno, H., Kouda, M., Kodama, T., Kojima, Y., Knodo, S., Konno, H., Kouda, M., Kodama, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Nagata, T., Niura, M., Mirra, M., Mirra, J., Miyazaki, A., Masuda, H., Matsubara, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, T., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osako, N., Otta, W., Otta, M., Ooka, M., Ooka, M., Ooka, M., Ooka, M., Ooka, M., Ooka, M., Ooka, M., Saico, K., Saitoh, K., Saico, K., Saicoh, K., Saico, K., Saicoh, K., Shibata, K., Shibata, K., Saico, K., Saicoh, K., Shibata, K., Saico, K., Saicoh, K., Shibata, K., Sugano, S., Shinagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Yosamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
                                                                                                                                   ramamoto, M.

PAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fais Genome Sequencing & Analysis Group: Otomo, M., Naira, J., Kobayashi, M., Miura, J., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Kayu, R., Sugamo, S., Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugamo, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K. Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, A., Hachakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Tida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Konda, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, T., Tomaru, A., Tagami, M., Tagami, Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
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Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head (Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (2-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007)
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japoni.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,B., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.
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sativa (japonica cultivar-group)"
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/organism="Oryza

33 Seralahathrvalproffirfhr	/mol_type="mRNA" /cultivar="Nipponbare" /db_xref="taxon:39947" /db_xref="taxon:39947" /clone="002-101-C10"  Alignment Scores:
Qy 329 GlykagolivalTyraewirglyfyraewirciuciuwyshlablanghlafyraep 348 1145 GGAAGCCAACTATATCTAGGTGTTATGCACCTAAGATAAGGTGCAGGGCTTATGAT 1204 349 LewhlablatelwsyftrglyproserthHisileseanthesecilegiusatty 368 1205 CTGGCTGCCCTGAAATACTGCGGCTTATGATAAACTAAGGTCCAGGGCTTATGAT 1204 349 ASSACRACTAAGATGCACCAGAATGCCAAGAATTACCCGTTAGAAAACTAC 1264 349 ASSACRACTAAGATGCACGAATGCAAAGAATGACAAGAATTACCGGTAGAAAACTAC 1264 349 ASSACRACTAGAAGATGCAAGAATGACAAGAATTACCGGGGAAATATAAACTAC 1264 349 ASSACRACTAGAAGATGCAAGAATGACAAGAATTACCAGGGAAAGAATTACCAAGAATTACAAGTACAAGAATTACAAGAAAAAACAAGAAAGA	Db 845 CAGTCCAGCAGCTGCGTCAGTGCAGCTCCCCAGCAGCATCAGCAGATGGCGGTGGTCGCT 904  Qy 270270  Db 905 GCAGCTGCTGCTGCTGGTGATGGCCAGGAACAGTAATGACGGTAGCAGCAGCAGCAT  QY 271LysLysArgGlyHisalalysLeuGlyGlnLysGlnProValHisArgLysGer 288  965 GTCGGGAAGAAGAGGGGCACCGGGAAAAGCAAGCAAGAGAAGTCC 1024  Qy 289 IleAspThrDheglyGlnArgThrSgThTyrArgGlyValThrArgHisArgTrpThr 308  Db 1025 ATTGACACGTTTGGGCAGACAGTACAGGACAGGCAACAGTTGACCAGGCAAGTTGCAACAGTTGAACAGTTGAACAGTTGAACAGTTGAACAGTTGAACAGTTGAACAGTTGAACAGTTATGLYS 328  Db 1085 GGAAGATATGAAGCCCACCTCTGGGATAACAGTTGAAAAAGGAACAGGAAAG 1144

	Query Match DB: US-10-024-6	Pred. No.: Score: Percent Sim Best Local								CDS		FEATURES source	JOURNAL	AUTHORS TITLE		SOURCE ORGANISM	ACCESSION VERSION	DEFINITION	RESULT 6	Db 20		Qy 6	ш		2y 5	Db 1856
13 GlyAsnAsnHi	~	. No.: 2 e: 2 ent Similarity: 5 Local Similarity: 4		FSVI AAAS	HLRF HAGT GGGA	DIAN KKRG	нни: курс	/tra_/db_	/codon /prote	1 /not			Patent: WO 02059332-A 8 Monsanto Technology LLC	He, S.S. and D	Eukaryota, Vi Spermatophyta Ehrhartoideae	Oryza sativa Oryza sativa	_	AX555223 Sequence 8 fr		72	. 15	635 TrpLeuProSe			98	
isAsnTrpLeuGlyi	23 (1-	2.48e~82 1349.50 57.32% 48.02%		-QDIVSTVDAAGAPI	KSSGFSRGASIYRO OGEAAEAYDVAAII AAAVADAAAALVQAO	NAAADDVCAAGPIII 3GADRAGQKQPVHRI	HHVHQHQQQHGGGI SSLCIMEALRGGDQI DDGGAVGGDPHHGGO	xref="REMTREMI nslation="MASC	codon start=1  protein id="CAD58228.1"  Ab wref="GI-25888752"	note="unnamed protein	nism="Oryza _type="unassi _tref="taxon:	Location/Qualifiers		and Dotson, S.B. acid molecules asso	kridiplantae, s a, Magnoliophyt e, Oryzeae, Ory		GI:25898751	201 From Patent WO02		GCTCATCTCCCTGTTTTTGCAGCCTGGACAGAT	reccesces and reccessors	rpLeuProSerProThrValGIn-		Thrivelleval	:rArgGluAlaSerI          GAGGGAGGGGAGCO	GAAGATCAGTGGC <i>I</i>
GlyAsnAsnHisAsnTrpLeuGlyPheSerLeuSerProHisMet-LysMetGluAla	Indels: Gaps: (1-2010)	Length: Matches: Conservative: Mismatches:		fsvlodivstvdaagaperapemsmaatslgnskeosporgggsgggvlatlfarp aaaskiyspvplntwaspspavssvparagvsiahlpmfaawtda"	HLRRKSSGFSRGASI YRGVTRHIQHGRWQARIGRVSGNKDL YLGTFI ASAFAAARRAR HAGTQEEAAEA YDVAAI KFRGLMA VTNFDITRYDVDKI LESSTLLPGELARRKGKVGD GGGAAA VADAAAAL VQAGNVAEWKMATAAAL FAAARTEQQQQHGHGGHQHHDLLPSDA	DIANAAADDVCAAGPIIFTGGHLHPLTLSMSSAGSQSSCVTVQAAAAGEPYNAMDAVS KKRGGADEAGQKQPVHRKSIDTGGGRTSQXRGVTRHRWTGRXEAHLMNNSCKKEGG)TR KKROVYIGGYNWEEKAARAYNIAALTWGESTHINDPLETVOEELRAMKNASCKYVA	HHHHHHVHQHQQQHGGGLFYNPAAVASSFYYGGGHDAVVTSAAGGGSYYGAGFSSMPL KSOGSLCIMEALKGGDQEQQGVVVSASFKLEDFLGAGAMALSLDMASFYYGGHGHHQ GHAQDGGAYGGDDHHGGGGFLOCAVFDFAGAGHDAAIVHDGSAAVVAGGGY	3L:CAD58228" NSSSSSGSMAATAG	3228 . 1 <sup>1</sup>	mtein product"	sativa" igned DNA" \$530"	66	01-AUG-2002; (US)	associated with pl	Eukaryota, Viridiplantae, Streptophyta, En Spermatophyta, Magnoliophyta, Liliopsida, Ehrhartoideae, Oryzeae, Oryza.			2010 bp DNA WO02059332.		CCTGGACAGAT 2104			-CATCCCACCGCCGTCAGCCTCGCCGCCATGAACCCC	DroDroMetGlijThrIveIleValBanDroIleGlvThraerValThraer	LeuserserserargGluAlaserProGluLyeArgGlyProSerLeuLeuPheProMet        :::	GTCCCGGGAGGGAAGATCAGTGGCATCAACTTCTCGAACTCGTCTTCGCTGGTGACTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-JUN-2002) Plant Gene Expression Center, 800 Buchar Street, Albany, CA 94710, USA.
The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA); RIKEN Arabidopsis Full-Length CDNA'); Seki,M., Narusaka,M., Ishida, Satut,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                                                                                                                                                                                                                              /organism="Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                  /gene="At4g37750"
                                                                                                                                                                                       /ecotype="Columbia"
/note="This clone i
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Qy       158 ThrHisProTyrTyrSerGlyLeuAlaCysHisGlyLeuTyrGlnAlaProLeuGluGlu       177         Db       499		SerProSerGlnSerHisLeuSerAsnPheGlyWetCysTyrGlyValGlyGluAsnGly 63  GGTGACAACACTACTTTTGTTTTTTTTTTTTTTT	-10-024-632- 1 1 21 61 30	Alignment Scores: 5.71e-B1 Length: 1699 Pred. No.: 1328.00 Matches: 312 Score: 1328.00 Matches: 312 Percent Similarity: 52.84% Conservative: 69 Best Local Similarity: 43.27% Mismatches: 116 Query Match: 37.92% Indexs: 224 DB: Gaps: 21	/protein_id="AAM51282.1" //db_xref="G1:21436287" //db_xref="G1:21436287" //translation="MKSPCONDDNUHSNTTNLLGEGLSSNNMKNMGGRGGRGALYSSST //translation="MKSPCONDDNUHSNTTNLLGEGLSSNNMKNMGGRGGRGALYSSST SSASNTSSSSVPPQLVVGDNTSNFGVCYGSNPNGGIYSHMSVMPLRSDGSLCLMEALNR SSHSNHHQDISSPKVEDFFGTHNNTSHKEAMDLSLDSLFYNTTHEPTTTNFQEFFSF PQTRNHEETRAYGNNPSLTHGGSFNVGVVGFGSQSSCTIGSHHHQQ NQNQNHQSQNHQQISBALVETSVGFETTTMAAAKKKRQQEDVVVVGQKQIVHRKSIDT FGQRTSQYRGFTHTNFSARNYQKEIEDMGMVTKGFVLAGTVNGKGKARAYDL AALKYMGFSTHTINFSARNYQKEIEDMGMVTRQEYVALIRKKSSGESRGAJYTGFVTH HQHGRWQARIGRVAGNKULYLGTFGTQEEAAEAYDVAAIKFKSGESRGAJYTGFVTH HQHGRWQARIGRVAGNKUNSIVRNTEDOTALNAVVEGGSNKEVSTPERLLSFPAIFA LPQVNQKMFGSNMGGNMSFWTSNPNAELKTVALTLPQMPVFAAWADS" 1669. 1699 /gene="At4g37750"
1402 506 1429 526 1432	Oy  426 LeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGluAlaTlaAla 445  [H]	Qy 366 GluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArgGlnGluTyrValAla 385		Qy 269 ASDAIALYSLYSARGGIYHISAlaLYSLEUGIYGINLYSGINDROVAHHIS 285	Qy 218 GlnGlnMetAsnCysGlyMetGlyAsnGluArgAsnGlyValSerLeuGlySerValGly 237

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GCTCTAAATGCT-----

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IleMetAsnCysGlyAsnTyrArgAsnSerAlaPheSerMetAlaLeuGlnAspLeuIle

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1 (bases 1 to 1905)

Elliott,R.C., Betzner,A.S., Huttner,E., Oakes,M.P., Tucker,W.Q., derentes,D., Perez,P. and Smyth,D.R.
AINTEGUMENTA, an APETALA2-like gene of Arabidopsis with pleiotropic roles in ovule development and floral organ growth
Plant Cell 8 (2), 155-168 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (thale cress)
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Arabidopsis thaliana ANT (AINTEGUMENTA) mRNA,
                                                                                                                                                                                                                                                                         Submitted (27-NOV-1995) David Smyth, Genetics and Dev. Biology, Monash University, Wellington Road, Clayton, VIC 3168, Australia Location/Qualifiers
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Accession Number U12546"
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            GlyLeuLysAsnTrpValAlaProThrArgGluPheSerThrHisGlnGlnValLeuGlu 217
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/gene="AINTEGUMENTA"
/note="ecodes second AP2
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SSHSNHHQDSSPKVEDPFGTHHINNTSHEAMDLSLDSLFYNTTHEPNTTNFGSFFSF
PQTRNHEEETRNYGNDPSLTHGGSFNVGVVGEFGQSLSLSSLFYNTTHEPNTTNFGSFFSF
PQTRNHEEETRNYGNDPSLTHGGSFNVGVVGEFQQSLSUSGPSGSSCSTGSHHQQ
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HQHGRWQARIGRVAGNKDLYLCTFGTQBEAAEAYDVAAIKFRGTNAVTNFDITRYDVD
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RIMSSNTLLSGELARBNNNSIVVRNTEDQTALNAVVBGGSNKEVSTPERLLSFPAIFA LPQVNQKMFGSNMGGNMSPWTSNPNAELKTVALTLPQMPVFAAWADS"

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AspPheLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGluArgGly---103 388

GATTTCTTTGGG------ACCCATCACAACAACAAGTCACAAAGAAGAAGCCATG 436

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AspLeuLeuSerGlnProPhe------ArgGlnGlnGlyHisMetSerValGln 157 ACTACAAACTTTCAAGAGTTCTTTAGCTTCCCTCAAACCAGAAACCAT-487 535

GluThrThrLysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGlu 197 ThrHisProTyrTyrSerGlyLeuAlaCysHisGlyLeuTyrGlnAlaProLeuGluGlu -CCTAGTTTGACACAT GAGGAA 177 541

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526 ValLeuPheAsnHisProSerGlnGlnGlnGlnAlaAsnGlyAsnGlySerAspGlnLys 545	1328 ATTAAGTTCCGTGGCACAATGCTGTGACTAACTTTGATATCACGAGGTACGATGTTGAT 466 ArgIlemetalaSerSerAsnLeuLeuAlaGlyGluLeuAlaArgArgLysLysAspAsn 485 [	406 ArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgValAlaGlyAsnLyAsnLyAsp 425	1028 GCATATGATCTTGCTGCACTAAGTACTGGGGTCCCTTACTCACCAATTTTCTCTGCG 1087  366 GIUASHTYYGIRVAIGINLEUGIUGIUMELLYSASHMELSEYAYGGINGIUTYTVAIAla 385	σωση σου	262 ASPAIALYSLYSARGCITTGTGGAGACAAGCGTTGGGTTTGAGACGACGACAATGGCGCT 787 269 ASPAIALYSLYSARGGIYHISAlaLySLEUGIYGINLYSGINProValHis 285	81 GGA  18 GlnGlnMetAsnCysGlyMetGlyAsnGluArgAsnGly
Alignment Scores: 6.9e-81 Length: 1955 Pred. No.:	/produce "CKC" /produce "CKC" /produce "CKC" /produce "CKC" /produce "CKC" /produce "CKC" /produce "CKC" /produce "CKC" /produce "CKC" /produce "CKC" /broduce "MKSFCDNDNNHSNTTNLGESLSSNMMKNGGRGGREAIYSGST /broduce "MKSFCDNDDNTSNFGVYGSNDGGIYSHMSVMPLRSDGSLCIMGSLING SSHSNHHOOS PKVEDFFGTHHNGTSHKEAMDLSLLSMSFGSOSSCITGSHHOO POURHOSONHOSSONHOSSYEAHNDNSFYAAAKKKRGOEDVVVGGIYHRKSIDT FGGRTSQYRGVTHHRWTGSYEAHNDNSFYAAAKKKRGOEDVVLGGYDMEEKAARAYDL FGGRTSQYRGVTHHRWSAENYQKEIEDMKNVTRQEYYAHLRRKSGFSRGASIYRGVTNH HALKYWGFSTHTWFSAENYQKEIEDMKNVTRQEYYAHLRRKSGFSRGASIYRGVTNH HALKYWGFSTHTWFSAENYQKEIEDMKNVTRQEYYAHLRRKSGFSRGASIYRGVTNH HALKYWGFSTHTWFSAENYQKEIEDMKNVTRQEYYAHLRKSGFSRGASIYRGVTNH HALKYWGFSTHLSGELARNNSIVYRNTEDQTALNAVVEGGSNKEVSTPERLLSFPAIFA LPQVNQKMFGSNMGGNMSFWTSNFNAELKTVALTLPQMFVFAAWADS"	FEATURES Location/Qualifiers  11955  80urce /organism="Arabidopsis thaliana" /mol_type="mRNA" /db xref="taxon:3702" /db xref="taxon:3702" /function="transcription factor; complements a yeast protein kinase C 1 mutant; Method: conceptual translation supplied by author." /codon start=1	Arabidopsis thaliana (thale cress)  ORGANISM Arabidopsis thaliana (thale cress)  Arabidopsis thaliana (thale cress)  ORGANISM Arabidopsis thaliana (thale cress)  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  rosids; eurosids II, Brassicales; Brassicaceae; Arabidopsis.  REFERENCE 1 (bases I to 1955)  AUTHORS Vergani, P., Morandini, P. and Soave, C.  TITLE Direct Submitssion  JOURNAL Submitted (29-DEC-1995) Paola Vergani, Dept. of Biology 'L.  Gorini', University of Milan, Via Celoria 26, Milan, 20133, Italy	Cy 663 Thr 663  Db 1700 TCT 1702  RESULT 9 ATU44028 ATU44028 ATU44028 DEFINITION Arabidopsis thaliana transcription factor CKC mRNA, complete cds. ACCESSION U44028.1 GI:1171428  VERSION U44028.1 GI:1171428	1523 ACTO 624 IleV 625 ATGT 1583 ATGT 643 Met#	

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Qy 606 ProGlutysArgGlyProSerLeuLeuPheProMetFroProMetGlufintlys 623	ThrHisPheSerAsnThrSerSerLeuValThrSerLeuSerSerSerArgGluAlaSer 605	1516 GCTCTAAATGCT	526 ValLeuPheAsnHisProSerGlnGlnGlnGlnAlaAsnGlyAsnGlySerAspGlnLys	Db 1477	Qy 466 ArglieMetAlaSerSerAsnLeubenAlaClyGlübenAlaArgArgLysiysAspAsn 485	446 IleLysPheArgGlyAlaAsnAlaValThrAsnPheAspIleSerArgTyrAspValGlu	Oy 426 LeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGluAlaTyrAspValAlaAla 445	Qy 406 ArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgValAlaGlyAsnLysAsp 425	OY 386 HISLGUARGARGLYSSERSERGLYPHESERARGGLYALASERILETYRARGGLYVALTH 405	Oy 366 GluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArgGlnGluTyrValAla 385	Oy 346 AlaTyrAspLeuAlaAlaLeuLysTyrTzpGlyProSerThrHisIleAsnPheSerIle 365	Qy 326 ThrargLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGluGluLysAlaAlaArg 345 :::	Oy 306 ArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCysLysLysGluGlyGln 325	Qy 286 ArgLysSerIleAspThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgHis 305	Db 826 GCGAAGAAGAAGAGGGACAAGAGGATGTTGTAGTTGTTGGTCAGAAACAGATTGTTCAT 885

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Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Garninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kam, Ya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                           The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAS: Yamada, K., Banh, J., Chann, E., Chang, E., Dale, J.M., Deng, J.M., Galdsmith, A.D., Lee, J.M., Cnodera, C.S., Quach, H.L., Tang, C.C., Goldsmith, M., Wu, H.C., Xamamura, Y., Yu, G., Boweer, L., Chen, H., Chenk, R., Jones, T., Karlin-Namn, G., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (19-FBB-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs (FAFL CDNA: TKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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2 (bank, M., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Pamada, K., Banh, J., Chan, M., Onodera, C.S., Quach, H.L., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Lam, B., Gones, T., Kamiya, A., Karilin-Rumann, G., Kawaii, K., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinnzaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                      Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.
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                                                                                                                                                                             Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.
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                                                                                                                                                    ocation/Qualifiers
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278 TCATCTTCAACTTCTTCAGCTGCAACTTCTTCTTCTTCTTCTTCTACCTCAACTTGTTGTTT
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GATCTTAGCTTAGATAGTTTATTCTACAACACCACTCAT-----
                                                                                                                                                                                                                                                                                                                                                                    GGAATCTATTCTCACATGTCTGTGATGCCACTCAGATCTGATGGTTCTCTTTATTG
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                                                          ---LeuSerLeuAspSerIleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArg 141
                                                                                                                                                                                   AspPheLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGluArgGly---
                                                                                                                                                                                                                                                     GAAGCTCTCAACAGATCTTCTCACTCGAATCACCATCAAGATTCATCTCCAAAGGTGGAG
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RIMSSNTLLSGELARRNNNSITVRNTEDQTFALMAVVEGGSUGEVSTPERLLGFPAIFA
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(Lambda ZAP) as a XhoI/SstI insert."
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426 LeuTyrLeuGlyThrPheSerThrGinGluGluAlaIGluAlaTyrAsgValAlaAla 445	HISLEMATGATGJYBSEFSETGJYFRESETATGGJYALASETI ETYKALGGIYGIJYGLIHILI HISLEMATGATGGJYBSEFSETGJYFRESETATGGJYALASETI ETYKALGGIYGIJYGLIHILI HISLEMATGATGAGAGAGTCACA CATTTGAGAAGGAAGAGAGAGTGGTTCTCTAGGGGTGCTTCCATCTATAGAGGAGTCACA ATGHISHISGINHISGIYALGTTPGINALAALGILIGGIYALGYVALAGAGATLGGAAACAACAA ATGHISHISGINHISGIYALGTTPGINALAALGATGGTAGAGTCGCTGGAAACAAAGAT AGACATCACCAGCATGGAAGGTGGCAAGCACGGATTGGTAGAGTCGCTGGAAACAAGAT	46 ALITYRSDLECHIAN ABLEUN/STYTIPGLYFTOSETITE 46 ALITYRSDLECHIAN ABLEUN/STYTIPGLYFTOSETITE 47 ALITYRSDLECHIAN ABLEUN/STYTIPGLYFTOSETITE 48 GCATATGATCTTGCTGCACTCAAGTACTGGGGTCCCTCTACTCACACCAATTTCTCTGCG 48 GCATATGATCTTGCTCCAAGTACTGGGGTCCCTCTACTCACACCAATTTCTCTCTGCG 66 GLUASHTYTGLNVALGLUAGACATGAAGAACATGACTAGACAAGAATATGTTGCA 66 GLUASHTYTCAGAAAGAGATTGAAGACATGAAGAACATGACTAGACAAGAATATGTTGCA 67 ALITYRSDLECHIAN ABLECTICACTAGACAAGAATATGTTGCA 68 GAGAATTATCAGAAAGAAGATTGAAGACATGAAGAACATGACTAGACAAGAATATGTTGCA 69 GAGAATTATCAGAAAGAAGATTGAAGACATGAAGAACATGACTAGACAAGAATATGTTGCA	28 AGATGGACTGGTAGATATGAAGCTCATCTATGGGACAATAGTTTCAAGAAGGAAG	ArgLysSerIleAspThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgHis	262	Thralaproser	701 GGA 703 701 GGA 703 218 GlnGlnMetAsnCysGlyMetGlyAsnGlyAsnGlyValSerLeuGlySerValGly 237 218 GlnGlnMetAsnCysGlyMetGlyAsnGluArgAsnGlyValSerLeuGlySerValGly 237 704 GGGTCTTTAATGTAGGGGTATATGGGGAATTTCAA	142 AspLeuLeuserGlnProPheArgGlnGlnGlyHisMetSerValGln 157
	AUTHORS TITLE JOURNAL COMMENT	VERSION VERSION KEYWORDS SOURCE ORGANISN	Db 18 RESULT 11 BD274516 LOCUS DEFINITION	& B &	לם עס לם	\$ \$ \$ \$	δ dd δ	B & B & B & B
PD 15-CCT-2002  PF 07-JAN-2000 JP 2000592392  PF 08-JAN-1999 US 09/227421  PI ROBERT L FISCHER, YUKIKO MIZUKAMI  PI ROBERT L FISCHER, YUKIKO MIZUKAMI  CC encodes first AP2 domain  CC encodes linker region  CC encodes second AP2 domain	Pischer, L. and Mizukami, Y.  Pischer, R.L. and Mizukami, Y.  Methods for modifying weight of organ, controlling fertility and enhancing asexual reproduction in plant Patent: JP 2002534078-A 1 15-OCT-2002;  THE REGENTS OF THE UNIVERSITY OF CALIFORNIA OS Arabidopsis thaliana (thale cress)  PN JP 2002534078-A/1	DE274516.1 GI:33084284  JP 2002534078-A/1.  Arabidopsis thaliana (thale cress)  Marabidopsis thaliana  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Ñ	643 MetArgProSerProAlaIleSerLeuSerHisLeuProValPheAlaSerTrpThrAsp 662 1763 CTTAAGACCGTCGCTCTTACTTTGCCTCAGATGCCGGTTTTCGCTGCTTGGGCTGAT 1819 663 Thr 663	1643 ACTCCCGAAGAGACTCTTGAGTTTTCCGGCGATTTTCGCGTTGCCTAAGTTAATCAAAAG 1702 624 IleValAsnProIleGlyThrSerValThrSerTrpLeuProSerProThrValGln 642 ::: :::	1609 1609  586 ThrHisPheSerAsnThrSerSerLeuValThrSerLeuSerSerSerAsrgGluAlaSer 605	46 IleMetAsnCysGlyAsnTyrArgAsnSerAlaPheSerMetAlaLeuGlnAspLeuIle 5 98 GCTCTAAATGCT	:::    :::     :::

773 198 812 218 815	ArgGlnGlnGly CCCTCAAACCAGAAAC SHisGlyLeuTyrGln	Db 560 GAAGCTCTCAACAGATCTTCTCACTCGAATCACCATCAAGATTCATCTCCAAAGGTGGAG 619  Qy 104 AspPheLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGluArgGly 122	Qy 44 SerProSerGlnSerHisLeuSerAsnPheGlyMetCysTyrGlyValGlyGluAsnGly 63	21 PheSerLeuSerProHisMetLygMet	-10-024-632-2 (1-663) x BD274516 (1-2148)    MetLysArgIleAsnGluSerAsnAsnThrAspAspGlyAstrickitis:::::::::::::::::::::::::::::::::::	Alignment Scores: 7.84e-81 Length: 2148 Pred, No.: 7.84e-81 Length: 312 Score: 1328.00 Matches: 312 Percent Similarity: 52.84% Conservative: 69 Best Local Similarity: 43.27% Mismatches: 116 Query Match: 37.92% Indels: 224 DB: 6 Gaps: 21	FH Key Location/Qualifiers FT CDS (269)(1936) FT misc_feature (1109)(1339) FT misc_feature (1340)(1414) FT misc_feature (1415)(1621). FEATURES Location/Qualifiers Source 12148
Qy 526 ValLeuPheAsnHisProSerGlnGlnGlnGlnAlaAsnGlyAsnGlySerAspGlnLys 545	406 AT GLEMECKA SHE SHE KARLEUL GUAL GUL YEL YEKA SHE KARLEUL GUAL GUL YEL YEKA SHE KARLEUL GUAL GUL YEL YEKA SHE KARLEUL GUAL GUL YEL YEKA SHE KARLEUL GUAL GUAL GUAL GUL YEL YEKA SHE KARLEUL GUAL GUAL GUAL GUAL GUAL GUAL GUAL GU	426 LeuTyrLeuGlyThrPheSerThrGlnGluAlaAlaGluAlaTyrAspValAlaAlaAlaGluAlaTyrAspValAlaAlaAlaGluAlaAlaGluAlaTyrAspValAlaAlaAlaGluAlaGluAlaAlaGluAlaAlaAlaGluAlaAlaAlaGluAlaAlaAlaGluAlaAlaAlaAlaGluAlaAlaAlaGluAlaAlaAlaAlaGluAlaAlaAlaAlaGluAlaAlaAlaGluAlaAlaAlaAlaGluAlaAlaGluAlaAlaGluAlaAcTTTTGGAACCTAGAAGCTGCAAAGCTTACGATGAAGCAGCACAAGCTTACGAAGCTACGATGAAGCAGCAGAAGCTTACGAAGTTACAGAAGTTACAGAGGTACGATGTTGATAAGTTCCGTGGCACAAATGCTGTGACTAACTTTGATAACAACAGAGGTACGATGTTGATATGATACACGAGGTACGATGTTGATATGATACACGAGGTACGATGTTGATATGATACACGAGGTACGATGTTGATATGATATGATAGATTAGATAGA	1319 GAGAATTATCAGAAAGAGATTGAAGACATGAAGAACATGACTAGACAAGAATATGTTGCA 386 HisLeuArgArgLysSerSerGlyPheSerArgGlyAlaSerIleTyrArgGlyValThr	Oy 326 ThrargLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGluGluLysAlaAlaArg 345 :::	Db 1079 AGAAAATCTATCGATACTTTTGGACAACGAACTTCTCAATACCGAGGCGTTACAAGACAT 1138  Qy 306 ArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCysLysGluGlyGln 325	59 CAGATCTCTGAAGCTCTTGTGGAGACAAGCGTTGGGTTTGAGACGACGACAATGGCGCT 69 ASDAlaLysLysArgGlyHisAlaLysLeuGlyGlnLysGlnProValHis	Qy 238 CysGlyGluLeuGlnSerLeuSerLeuSerMetSerProGlySerGlnSerSerCysVal 257

Db 329 TTCTCATTGTCTTCAAATATGGAAGTAGAAGGTAGAAGAAGCTATTTAC 388  Qy 30	US-10-024-632-2 (1-663) x AR316367 (1-2148)  Qy	Alignment Scores: 7.84e-81 Length: 2148 Pred. No.: 1328.00 Matches: 312 Score: 1328.00 Matches: 312 Percent Similarity: 52.84% Conservative: 69 Best Local Similarity: 43.27% Mismatches: 116 Query Match: 37.92% Indels: 224 DB: Gaps: 21	JOURNAL Patent: US 659357-A1 106-MAY-2003; FEATURES: Location/Qualifiers source 12148 //organisme"unknown" ORIGIN	Unknown.  Unknown.  Unclassified.  Unclassified.  1 (bases 1 to 2148)  Fischer, R.L. and Mizukami, Y.	RESULT 12 AR316367 AR316367 AR316367 DEFINITION Sequence 1 from patent US 6559357. ACCESSION AR316367 VERSION AR316367.1 GI:31711158	Oy 663 Thr 663 Db 1931 TCT 1933	1814 ATGTTCGGATCAAATATGGGCGGAAATATGAGTCCTTGGACATCAAACCCTAATGCTGAG 643 MetArgProSerProAlaIleSerLeuSerHisLeuProValPheAlaSerTrpThrAsp :::::         :::::	Db 1720 1720  Qy 586 ThrHisPheSerAsnThrSerSerLeuValThrSerLeuSerSerArgGluAlaSer 605  Qy 606 ProGluLysArgGlyProSerLeuLeuPheProMetproProMetGluThrLys 623  Qy 606 ProGluLysArgGlyProSerLeuLeuPheProMetproProMetGluThrLys 623  Qy 674 IleValAsnProlleGlyThrSerValThrSerTrDLeuProSerProThrValGln 642
346 AlaTyrAspleuAlaAlaLeuLysTyrTrpGlyProSerThrHisIleAsnPheSerIle	Oy 306 ArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCysLysGluGlyGln 325	Qy 269 AspAlaLysLysArgGlyHisAlaLysLeuGlyGlnLysGlnProValHis 285	Qy 258 ThrâlaProSer 261	Db 815 GGGTCTTTÄÄTGTÄĞGĞGTÄTATGGGĞÄÄTTTCÄÄ	198 GlyLeuLysAsnTrpValAlaProThrArgGluPheSerThrHisGlnGlnValLeuGlu 	178 GluThrThrLysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGlu	Qy 142 AspLeuIeuSerGlnProPheArgGlnGlnGlyHisMetSerValGln 157	

SOURCE ORGANISM ORGANISM REFERENCE AUTHORS TITLE TOURNAL FEATURES SOURCE	Qy  Db 1  RESULT 13 AR427901 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS	0 dy 04	B & B & B &	5	QV DB QQ	<u> </u>
Unknown.  SM Unknown.  Unclassified. 2148)  E 1 (bases 1 to 2148)  Fischer, R. L. and Mizukami, Y.  Methods for altering organ mass, controlling fertility and enhancing asexual reproduction in plants  L Patent: US 6639128-A 1 28-OCT-2003;  Location/Qualifiers  rce 1. 2148	663 Thr 663 1931 TCT 1933 3 3 AR427901 2148 bp DNA linear PAT 18-DEC-2003 N Sequence 1 from patent US 6639128. N AR427901 AR427901.1 GI:40186930	4 4 2 4	20		466 ArgIleMetAlaSerSerAsnLeuLeuAlaGlyGluLeuAlaArgArgLysLysAspAsn 485	406 ArgHisHisGlnHisGlyArgTrpGlnAlaArgTleGlyArgValAlaGlyAsnLysAsp 425
8 2 8 2 3 8 1 5 2 3 8 9 9 9 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5	Qy 178 GluThrThrLysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGlu 197	668 GATCTTAGCTTAGATAGTTATTCTACAACACCCACTCAT:  142 ASpLeuLeuSerglyDropheArgGlnGlnGlyHisMetSerValGln	84 GluAlaLeuLysArgSerGlnThrGlnValMetValProThrSerSerProLysLeuGlu 1	Qy  30GluAlaThrSerAlaAlaThrYalProThrThrPheTyrMet 43  389 TCATCTTCAACTTCTTCAGCTGCAACTTCTTCTTCTTTCT	US-10-024-632-2 (1-663) x AR427901 (1-2148)  QY	/organism="unknown" /mol_type="genomic DNA"  Alignment Scores: 7.84e-81 Length: 2148 Pred. No.: 1328.00 Matches: 312 Score: 52.84* Conservative: 69 Percent Similarity: 52.84* Mismatches: 116 Query Match: 37.92* Indels: 224 DB: 6 Gaps: 21

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1720 1720 586 ThrHisPheSerAenThrSerSerLeuValThrSerLeuSerSerSerArgGluAlaser 605	CAGATCTCTGAAGCTCTTGTOGAGCAAGCGTTGGGTTTGAGCGCTGGGCGACAACCACTTCGACACCACTTGAGCACCACCACCACCACCACCACCACCACCACCACCACC	01:00:00:00:00:00:00:00:00:00:00:00:00:0
Alignment Scores: 7.84e-81 Length: 2148 Pred. No.: 1328.00 Matches: 312 Score: 1328.00 Matches: 312 Percent Similarity: 52.84% Conservative: 69 Best Local Similarity: 43.27% Mismatches: 116 Over Matches: 27, 27, 27, 27, 27, 27, 27, 27, 27, 27,	1754 ACTCCCGG 624 IleVal- 1814 ATGTTCG 643 MetArgp 1874 CTTAAG- 663 Thr 663 1931 TCT 193 1931 TCT 193 ATU40256 U40256 U40256 I Arabidops Complete U40256 I Arabidops Spermacop rosids, e 1 (bees Sperm	Qy 606 ProGluLysArgGlyProSerLeuLeuPheProMetBroProMetGluThrLys 623

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	Qy 269	Qy 262 Db 959		Оу 258		Db 815		Qy 198		Qy 178		Оу 158		Qy 123 Db 668			Qy 84	Db 500	4.		ω <sup>.</sup>	Ov 30		Qy 1 Db 269	US-10-024-632-2 (1-663)	DB:
rgLysSerIleAspThrP	AspAlaLysLysArgGlyHis           	AGATCTCTGAAGCTCTTG	  crescrereaceaceace	ThrAlaProSer	ysGlyGluLeuGlnSerL 	GGGTCTTTAATGTAGGGGTATATGGGGAATTTCAA-	lnGlmMetAspCysGlyM	GlyLeuLysAsnTrpValA      GGA	GAAACTAGAAATT	luThrThrLysGluThrH		hrHisProTyrTyrSerG	AspLeuLeuSerGlnProPhe-	LeuSerLeuAspSerI             GATCTTAGCTTAGATAGTT	GATTTCTTTGGG	spPheLeuGlyGlyAlaT	luAlaLeuLysArgSerG	SHPHEMISSEPPICHEUI::::::::::::::::::::::::::::::::::::	GTGACAACA	erProSerGlnSerHisL	CATCTTCAACTTCTTCAG	TOTCHITGICTICHMAIN	PheSerLeuSerProHisMetLysMet	etLysArgIleAsnGluS             GAAGTCTTTTTGTGATA	(1-663) x ATU40256	<b>∞</b>
ArgLysSerIleAspThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgHis		GlyThraspSerValAlaVal 	   ACTGGCTCTCACCACCACCAACAAAACCAAAACCAAAAACCAAAAGCCAAAAGCCAAAAACCACC		CysGlyGluLeuGlnSerLeuSerLeuSerMetSerProGlySerGlnSerSerCysVal	::: GTATATGGGGAATTTCAA	GlnGlnMetAsnCysGlyMetGlyAsnGluArgAsnGlyValSerLeuGlySerValGly	GiyLeuLysAsnTrpValAlaProThrArgGluPheSerThrHi 	AGAAATTACGGGAATGAC	GluThrThrLysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGlu		ThrHisProTyrTyrSerGlyLeuAlaCysHisGlyLeuTyrGlnAlaProLeuGluGlu		LeuSerLeuAspSerIleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArg               :::::       :::   CTTAGCTTAGATAGTTTATTCTACAACACCACTCATGAGCCCAACACG	ACCCATCACAACAAC	AspPheLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGluArgGly	GluAlaLeuLysArgSerGlnThrGlnValMetValProThrSerSerProLysLeuGlu           	ABIRIDAD TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL THE T	CTAGCAACTTTGGTGTTTGC	SerProSerGlnSerHisLeuSerAsnPheGlyMetCysTyrGlyValGlyGluAsnGly	TCATCTTCAACTTCTTCAGCTGCAACTTCTTCTTCTTCTTCTTCCACCTCAACTTGTTCTT	IIVOALIUICILEANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	MetLysMet	MetlysArgIleAsnGluSerAsnAsnThrAspAspGlyAsnAsnHisAsnTrpLeuGly	6 (1-2148)	Gaps:
TyrArgGlyValThrArgHi:	-AlaLysLeuGlyGlnLysGlnProValHit ::::          PGTNGTTGTTGTTCNGANACNGATTGTTCN	-GlyThrAspSerValAlaVal 	CACCAAAGCCAAAACCACCAC	3001 CO COO T C T D O C T O C			/alserLeuGlyserValGl	ThrHisGinGinValLeuGlu	CCTAGTTTGÀCÀCAT	leuMetProGlnMetThrGlu		TyrGlnAlaProLeuGluGlu	ArgGlnGlnGlyHisMetSerValGln :::::	\laGluAlaGlnProAsnArg :::      GAGCCCAACACG	ACCCATCACAACAACACACAGTCACAAAGAAGCCATG	31ySerHisGluArgGly	ThrSerSerProLysLeuGlu	SATGGTTCTCTTTGCTTAATO	ratggatctaacccaaatgg \frac{1}{2} \frac{1}{2} CyrGlyValGlyGluAsnGly	TTCCACCTCAACTTGTTGTT	<i>Jaggir</i> cagaagc <i>ia</i> iiia <i>Ja</i> lprothrThrPheTvrMet		\snAsnHisAsnTrpLeuGl\ 		2 1	
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643	1814	1754	1721	586	1720	1709	546	1700	526	1697	1670	486	1619	1559	1499	426	1439	1379	386	1319	1259	346	1199	1139	306	1079
643	1814	1754	606 ProGluLysArgGlyProSerLeu	586	1720	1709	546	1700	526	1697	1670	486	1619	1559	1499	426	1439	1379	386	1319	1259	346	1199	1139	306	1079
Φ.	1814	1754 ACTCCCGA	1721	586 ThrHisPheSerAsnThrSerSerLe	1720	1709	546	1700	526	1697	1670	486 AspProArgAsnLysAspIleAspT	L	1559	1499			1379	386		1259			1139	306	

Qy 9 ASMTHYASPASPGLYASHASHASHASHTEPLEUGLYPHESETLEUSERPTOHISMET 27  Qy 9 ASMTHYASPASPGLYASHASHISASHTEPLEUGLYPHESETLEUSERPTOHISMET 27  16 GATAATGATGATAGTAATACGACTAATTTGCTAGGGTTCTCGTTGTTCAAATATGTTG 75  Qy 28LySMETGLUALATTYSERALATATTYCALPTOTHTTHEPHE 41  Qy 76 AAAATGGGTGGTGGAGAAGCTCTTTACTCATCTTCGTCGTTCTCAACATCTTCT 132  Qy 42 TYMETSETPCOSETGLISETHISLEUSERASPHEGLYMETCYSTY 57  Qy 42 TYMETSETPCACCACAGCTTGTTGTTGGCGACAACAGTAGCAACTATGGAGTTTGCTAC 189  Db 133TCTGTTCCACCACAGCTTGTTGTTGGCGACAACAGTAGCAACTATGGAGTTTGCTAC 189  Qy 58 G1YVA1G1YGlUASHG1YASHATGAATGTATCTCAAATGTCTGTGATGCCCCTCAGATCT 249  Db 190 GGTTCTAACTTAGCAGCTAGGGAAATGTATCTCAAATGTCTGTGATGCCCCTCAGATCT 249  77 ASPGLYSETLEUCYSILELEUGLUALALEULYSATGSET		pD 15-CCT-2002 pF 07-JAN-2000 JF 2000592392 pF 08-JAN-1999 US 09/227421 pI 08-DERT L FISCHER, YUKIKO MIZUKAMI pC A01H1/00, C12N5/10, C12N15/00, C12N15/00 CC BANT, ANT pC A01H1/00, C12N5/10, C12N15/00, C12N15/00 CC BANT, ANT pC A01H1/00, C12N15/10, C12N15/00, C12N15/00 CC BANT, ANT pC A01H1/00, C12N15/00, C12N15/00, C12N15/00 CC BANT, ANT pC A01H1/00, C12N15/00, C12N15/00, C12N15/00, C12N15/00 CC BANT, ANT pC A01H1/00, C12N15/00, C12N15/00, C12N15/00 CC BANT, ANT pC A01H1/00, C12N15/00, C12N15/00, C12N15/00 CC BANT, ANT pC A01H1/00, C12N15/00, C12N15/00, C12N15/00 CC BANT, ANT pC A01H1/00, C12N15/00, C12N15/00, C12N15/00 CC BANT, ANT pC A01H1/00, C12N15/00, C12N15/00, C12N15/00 CC BANT, ANT pC A01H1/00, C12N15/00, C12N15/00, C12N15/00 CC BANT, ANT pC A01H1/00, C12N15/00, C12N15/00, C12N15/00 CC BANT, ANT pC A01H1/00, C12N15/00, C12N15/00, C12N15/00 CC BANT, ANT pC A01H1/00, C12N15/00, C12N15/00, C12N15/00 CC BANT, ANT pC A01H1/00, C12N15/00, C1	Spermatophyta; Magnoliophyta; èudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  REFERENCE 1 (bases 1 to 1738)  AUTHORS Fischer, R. L. and Mizukami, Y.  Methods for moddifying weight of organ, controlling fertility and enhancing asexual reproduction in plant JOURNAL Patent: JP 2002534078-A 3 15-OCT-2002; THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  COMMENT DS Brassica napus (Tape)  DS Brassica napus (Tape)	RESULT 15 BD274518 LOCUS DEFINITION Methods for modifying weight of organ, controlling fertility and enhancing asexual reproduction in plant.  ACCESSION DE274518 VERSION VERSION SD274518 VERSION SD274518 VERSION SD274518 SOURCE SOURCE Brassica napus CRGANISM Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Db 1874 CTTAAGACCGTCGCTCTACTTTGCCTCAGATGCCGGTTTTCGCTGGGCTGAT 1930  Qy 663 Thr 663  Db 1931 TCT 1933
Oy  321 LystysGluGlyGlnThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGlu  B)  892 AAGAAGGAAGGTCATAGCAGAAAAGGAAGACAAGTTTATCTGGGGGGGTTATGATATGAGAG  951  952 GAGAAAGCTCATAGCAGAAAAGGAAGACAAGTTTATCTGGGGGGTTATGATATGAGAG  953 AAGAAGAAGGAAGGTCATAGCAGAAAAGGAAGCAAGTTTATCTGGGGGGTTATGATATGAGAG  954 GLUYSALAALATYAASpLeuALAALALEULySTYTTpGlyProSerThrHis  955 GAGAAAGCTGCTCGAGCATATGATCTTGCTGCACTCAAGTACTGAGTCCTCTACTCAC  1011  0y  361 IleasnPheserIleGluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArg  980  1012 ACTAATTTCTCTGTGGAGAATTATCAGAAAGAGATTGATGACATGAACATGACTCGA  1071  1072 CAAGAATATTTCTCTGTGGAGAATTATCAGAAAGAGATTGATGACATGAACATGAACATGACTCGA  1072 CAAGAATATGTTGCTCACTTGAGAAGAAAAACCAGTGGTTTCTCTAGGGGTGCTTCCATC  1071  1072 CAAGAATATGTTGCTCACTTGAGAAGAAAAACCAGTGGTTTCTCTAGGGGTGCTTCCATC  1071  1072 TYTATGGLYVAlThATGHISIGINHISGLYATGTTPGINALATGILGJUALAALAGTC  1071  1072 TATACAGGAGTCACCAGACATCACCAGCATGGAAGCTCGGAACCGTAGAGTC  1071  1072 TATACAGGAGTCACCAGACATCACCAGCATGGAAGCTCGGAACCGGTAGAGTC  1071  1072 TATACAGGAGTCACCAGACATCACCAGCATGGAAGCTCGGAACCGTAGAGTC  1191	281 772 301 832	Qy 227 GluargAsnG1yValSerLeuG1ySerValG1yCySG1YG1ULEUG1INSErLEUG 230	AspCysSerSerLeuMetProGlnMetThrGluGlyLeuLysAsnTrpValAlaProThr	127 403 147 454 167	Db 310 CATAGTCAAGTT

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Search completed: March 13, 2004, 07:10:13 Job time : 4737 secs

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits_-START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct_-THR_MAX=100
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct_-THR_MAX=100
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-MAXIEN=2000000000 -USER=US10024632_@CGN_1 1 164 @xunat_09032004_101210_10885
-MCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT_-DSPBLOCK=100 -
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-LONGLOG_-DEV_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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# ALIGNMENTS

RESULT 1 US-10-024-632-1

Sequence 1, Application US/10024632 Publication No. US20020170093A1

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GENERAL INFORMATION:
APPLICANT: He, Steve S.
APPLICANT: He, Steve S.
APPLICANT: He, Steve S.
APPLICANT: He, Steve S.
APPLICANT: He, Steve S.
APPLICANT: Detson, Stanton B.
TITLE OF INVENTION: GROWTH AND USES THEREOF
FILE REFERENCE: 38-21(51837)B
CURRENT FILING DATE: 200112-19
PRIOR APPLICATION NUMBER: US/10/24,632
CURRENT FILING DATE: 200112-19
PRIOR APPLICATION NUMBER: US 60/257,896
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1082 AAGCAGCCTGTGCATAGAAAATCTATCGACACATTTGGGCAAAGAACCTC	1022 TCTGGAACAGATTCTGTTGCTGTGGATGCAAAGAAGAGAGGGGCATGCTAAACTTG 1022 TCTGGAACAGATTCTGTTGCTGTTGGATGCAAAAGAAGAGGGGCATGCTAAACTTTG	962 TIACAGTCTCTAAGCTTATCTATGAGTCCTGGTTCTCAGTCTAGTTGTGTCACTGCT 261 SerGlyThrAspSerValAlaValAspAlaLysLysArgClyHisAlaLysLeuGly	902 AATTGTGGCATGGGCAATGAGAAATGGTGTGTGTTTTTAGGATCTGTGGGGTTGT 902 AATTGTGGCATGGGCAATGAGAAATGGTGTGTGTTTTTAGGATCTGTGGGGTTGT 241 LeuGlnSerLeuSerLeuSerMetSerProGlySerGlnSerSerCysValThri	pValAlaProThrArgGluPheSerThrHisdInGliV 	181 LysgluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGluGlyLeuLys 20	ACCTTCATTCACAACCTTCAGGCAACAAGGTCATATGAGTGTCCAAACACA TysserglyLeuAlacysHisglyLeuTyrglnAla?roLeuGluGluGluTh 	######################################	121 ArgGlyLeuSerLeu	101 LysLeuGluAspPh 	81 CyslleLeuGluAlaLeuLysArgSerGlnThrGlnValMetValProThrSet	61 GluasnGlyAsnPheHisSerProLeuThrValMetProLeuLysSerAspGlySer	A PheTyrmetSerProSerGlnSerHisLeuSerAsnPheGlymetCysTyr(	*UCUAL MANAI GAGGA MARKACUUSA (M. 1882) *Leuser ProHismet Lysmet Gluala Thrseral aala Thrval ProThrThr 4	-10-024-63	Bt Local Similarity: 100.00% Mismatches: ery Match: 100.00% Indels: ery Match: 13 Gaps:	res: 0 Length: 3502.00 Matches: 100.00% Conservative:	; OTHER INFORMATION: US-10-024-632-1
	641	621	01 SCHAGGARAGIA GARAGA	1922 581	m vo	1802	CY 501 SerValAsnAsnGluGluThrValGluValGluAlaGlyAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnA	B1 AIGHTHEATH AND AS THE ASSESSMENT OF THE ASSES	1622 AGATACGATGAGAGAGAATCATGGCCAGTAGCAATCTCCTCGCTGGGGAGCTTGCAAGG 1	4-1 177ASDVALALATIALISTISTISTISTISTISTISTISTISTISTISTISTISTI	421 AIGG YASHIYSASDIBOLY FIRE THE TOTAL THE TOTAL THE TOTAL YEAR OF THE TOTAL THE TOTA	401 TyrArgGdlyValinrakgHishisGillinsisyligii yolinalaaligii teliga ya ilinalaa ya ya ilinalaa ya ilina	381 1382	س سر	μω	Qy 321 LysLysGluGlyGlnThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGlu 340	Oy 301 GlyValThrArgHisArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCys 320

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US-10-424-599-136491
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Pred. No.:
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID MOS: 285684
SEQ ID NO 136491
LENGTH: 2405
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APPLICANT: Kovalic David K
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ORGANISM: Glycine max
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GluGluGluThrThrLysGluThrHisValSerAspCysSerSerLeuMetProGlnMet 195
                                                                           ValGlnThrHisProTyrTyrSerGlyLeuAlaCysHisGlyLeuTyrGlnAlaProLeu 175
                                                                                                                                                                                                                               TyrGlySerHisGluArgGlyLeuSerLeuAspSerIleTyrTyrAsnSerGlnAsnAla 135
                                                                                                                                                                                                                                                                                                                                                                TCTGATGGGTCACTTGGTATCTTGGAAGCTCTCAATAGATCACAAACGCAAGTGATGGTG 1098
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                                        GTCGARACACACCCTTATTACTCTGTATTTGCTTGTCGAGGTTTGTATCAGGCACCGTCG 1338
                                                                                                                        GAGGCTCAACCCAACAGAAACCTTCTTTCACATCCCTTCAGGCAACAAGGGCATGTGAAT 1278
                                                                                                                                                                                                     TATGGGAACCACGAGAGAGGTTTGAGCCTAGÁCAGCATCTATTATAACTCACAAAAACGCA 1218
                                                                                                                                                                                                                                                                                                                     ProThrSerSerProLysLeuGluAspPheLeuGlyGlyAlaThrMetGlyThrHisGlu 115
                                                                                                                                                                                                                                                                                                                                                                                        SerAspGlySerLeuCysIleLeuGluAlaLeuLysArgSerGlnThrGlnValMetVal
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                                                                                        454 ValThrAsnPheAspIleSerArgTyrAspValGluArgIleMetAlaSerSerAsn 472
                                                                                                                                                                                434
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                                                                                                                                         CAAGAGGAAGCAGAAGCATACGATGTAGCGGCGATCAAATTTCGCGGCGCAAATGCA 2346
                                                                                                                                                                           GlnGluGluAlaAlaGluAlaTyrAspValAlaAlaIleLysPheArgGlyAlaAsnAla 453
                                                                                                                                                                                                                                                                                                                                                                                 GAGGAAGCAGCAGAAGCATACGATGTAGCGCCGATCAAATTTCGCGGCCCAATGTCGTCA 2166
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Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Chou, Yihua
APPLICANT: Kovelic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cac, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 18711
LENGTH: 1378
TYPE: DNA
ORGANISM: Glycine max
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; OTHER INFORMATION: Clone ID: LIB3109-D11-F8_FLI
US-10-425-114-18711
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                                                                                                                                                            GAGGCTCAACCAGAAACCTTCTTTCACATCCCTTCAGGCAACAAGGGCATGTGAAT 756
                                                                                                                                                                                                                                                                               TyrGlySerHisGluArgGlyLeuSerLeuAspSerIleTyrTyrAsnSerGlnAsnAla 135
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GAGGAAGAAGCAACAAAGGAAACGCACGTT
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                                                                             GTCGAAACACACCCTTATTACTCTGTATTTGCTTGTCGAGGTTTGTATCAGGCACCGTCG 816
                                                                                                              ValGlnThrHisProTyrTyrSerGlyLeuAlaCysHisGlyLeuTyrGlnAlaProLeu 175
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                                                                                                                                                                                                  ; NAME/KEY: CDS; LOCATION: (25)..(2; OTHER INFORMATION: US-10-024-632-3
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US-10-024-632-2 (1-663) x US-10-024-632-3 (1-2323)
                                                       Query Match:
                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                           Pred. No.:
                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10024632

Publication No. US20020170093A1

GENERAL INFORMATION:

APPLICANT: Monsanto Technology LLC

APPLICANT: He, Steve 5.

APPLICANT: Dotson, Stanton B.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL PROLIFERATION

TITLE OF INVENTION: GROWTH AND USES THEREOF

FILE REFERENCE: 38-21(51837)8

CURRENT APPLICATION NUMBER: US/10/024,632

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: US 60/257,896

PRIOR RILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 3
LENGTH: 2323
                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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54.00%
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Matches:
                                                         Mismatches:
Indels:
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Qy 173 AlaProLeuGluGluGluThrThrLysGluThrHisValSerAspCysSerSerLeuMet 192	euTyrGln 1	Qy 133 GlnAsnAlaGluAlaGlnProAsnArgAspLeuLeuSerGlnProPheArgGlnGlnGly 152	43	rmetGLY 11	3 9	Qy 55 MetCysTyrdlyValdlyGluAsnGlyAsnthehlsserProLeuinrvalmet /2	TyrMetSerProSerGlnSerHisleu	GCTGCTGCTGCCGGAGCCATGTCGTCTCCTCCCGACAGCGCCACGACCTGCAACTTC	Db 73 CCGTCCTCTGAGCCATCGACTGCTGCTCATCATCATCATCATCATCATCCACCTGCT 132	AGCAACTGGT ThrValProT	-10-024-632-2 (1-663) x US-10-024-632-5 (1-1926)  13 GlyAsnAsnHisAsnTrpLeuGlyPheSerLeuSerProHisMetLysMetGluAlaThr	11afity: 46.45% MIBHACCHES: 40.22% Indels: 13 Gaps:	5.01e-142 1408-50 55.05%		; NAME/KEY: CUS ; LOCATION: (1)(1926) . OTHER INFORMATION:	; TYPE: DNA ; ORGANISM: Oryza Bativa ; ERATURE:	; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 5 ; LENGTH: 1926	; CURRENT FILING LATE: 2001-12-13; PRIOR APPLICATION NUMBER: US 60/257,896; PRIOR FILING DATE: 2000-12-21	; FILE REFERENCE: 38-21(51837)B; CURRENT APPLICATION NUMBER: US/10/024,632	; APPLICANT: Dotson, Stanton B. ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL PROLIFERATION ; TITLE OF INVENTION: GROWTH AND USES THEREOF	; APPLICANT: He, Steve S.
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US-10-024-632-2 (1-663) x US-10-024-632-8 (1-2010)  Qy	Alignment Scores: 1.32e-135 Length: 2010 Pred. No.: 1349.50 Matches: 351 Score: 1349.50 Matches: 351 Percent Similarity: 57.32% Conservative: 68 Pert Local Similarity: 48.02% Mismatches: 153 Best Local Similarity: 48.02% Mismatches: 163 Query Match: 38.54% Mismatches: 161 Query Match: 13 Gaps: 35	LOCATION: (1)(2010) LOCATION: (1)(2010) OTHER INFORMATION: 10-024-632-8		R OF SEQ ID NOS: 33 NOB: PatentIn version 3.1 NOB: PatentIn version 3.1 TH: 2010	5/10/024,632 -19 60/257,896	WIES ASSOCIATED WITH PLANT CELL PROLIFERATION A	No. US20020170093A1 ORMATION: Monsanto Technology LLC He, Steve S.	lication US/10024632.	651 LeuSerHisLeuProValPheAlaSerTrpThrAsp 662 :::               :::          1891GCTCATCTCCCTGTTTTGCAGCCTGGACAGAT 1923	635 TTpLeuProSerProThrValGlnMetArgProSerProAlaIleSer 650	618 ProProMetGluThrLysIleValAsnProIleGlyThrSerValThrSer 634  :::              ::: ::: 1795 CATCATCCCACCGCCGTCAGCCTCGCCGCCATGAACCCC 1833	598 LeuSerSerArgGluAlaSerProGluLysArgGlyProSerLeuLeuPheProMet 617 (	579 AspGluSerSerLysIleGlyThrHisPheSerAsnThrSerSerLeuValThrSer 597 (	559 MetAlaLeuGlnAspLeuIleGlyIleAspSerValGlySerGlyGlnHisAsnMetLeu 578 (	539 GlyAsnGlySerAspGlnLysIleMetAsnCysGlyAsnTyrArgAsnSerAlaPheSer 558 (	523 TrpLy8MetValLeuPheAsnHisProSerGlnGlnGlnGlnAlaAsn 538 (	
325 995 4	Oy 285 isArgLyeSerIleAspThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgH 305	OY 268 alaspala	QY 251 lySerGlnSerSerCyeValThr	Qy 239GlyGluLeuGlnSerLeuSerMetSerProG 251	Oy 221 snCysGlyMetGlyAsnGluArgAsnGlyValSerLeuGlySerValGlyCys 238	Qy 201 snTrpValAlaProThrArgGluPheSerThrHisGlnGlnValLeuGluGlnGlnMetA 221	Oy 181 ysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGluGlyLeuLysA 201 ;; ;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	Qy 162 yrSerGlyLeuAlaCysHisGlyLeuTyrGlnAlaProLeuGluGluGluThrThrL 181			Qy 105 eLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGluArgGlyLeuSe 124	Qy 87 8ArgserGlnThrGlnValMetValProThrSerSerProLysLeuGluAspPh 105	Qy 67 rProLeuThrValMetProLeuLysSerAspGlySerLeuCysIleLeuGluAlaLeuLy 87 ::::		Qy 48 rHis		

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1415 TCAACGCCGTCACCAACTTCGACATCACGAGGTACGACGTGGACAAGATCCTGGAGAGAGCA 1474
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                     ACCTGCCAATGTTCGCCGCGTGGACCGAC 2004
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                                                                                                          -----PheAsnHisProSerGlnGlnGlnGlnAlaAsnGlyAsnGlySerAspGlnL 545
                                                                isLeuProValPheAlaSerTrpThrAsp 662
                                                                                                                                                   rpLeu---ProserProThrValGlnMetArgProSerProAla---IleSerLeuSerH 653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-059-911-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10059911 Publication No. US20030159180A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (269)..(1936)
OTHER INFORMATION: Arabidopsis AINTEGUMENTA (ANT)
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                                                                                                                                                                                                                                                                                                                                                                                           449 GGT-----GACAACACTAGCAACTTTGGTGTTTTGCTATGGATCTAACCCAAATGGA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 TCATCITCAACTTCTTCAGCTGCAACTTCTTCTTCTTCTGTTCCACCTCAACTTGTTGTT 448
158 ThrHisProTyrTyrSerGlyLeuAlaCysHisGlyLeuTyrGlnAlaProLeuGluGlu 177
                                             719 ACTACAAACTTTCAAGAGTTCTTTAGCTTCCCTCAAACCAGAAACCAT-------
                                                                                                                                668 GATCTTAGCTTAGATAGTTTATTCTACAACACCACTCAT------GAGCCCAACACG 718
                                                                                                                                                            123 ---LeuSerLeuAspSerIleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArg 141
                                                                                                                                                                                                                                                             104 AspPheLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGluArgGly---
                                                                                                                                                                                                                                                                                                          560 GAAGCTCTCAACAGATCTTCTCACTCGAATCACCATCAAGATTCATCTCCAAAAGGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 ATGAAGTCTTTTTGTGATAATGATGATAATAATCATAGCAACACGACTAATTTGTTAGGG 328
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                                                                                                                                                                                                                                                                                                                                                GluAlaLeuLysArgSerGlnThrGlnValMetValProThrSerSerProLysLeuGlu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerProSerGlnSerHisLeuSerAsnPheGlyMetCysTyrGlyValGlyGluAsnGly
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                                                                                                                                                                                                                     GATTTCTTTGGG-----ACCCATCACAACACACAAGTCACAAAGAAGCCATG
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<u></u>	466 ArgileMetAlaSerSerAsnLeuLeuAlaGlyGluLeuAlaArgArgLysLysAspAsn 485 
ω	46 IleLysDheArgGlyAlaAsnAlaValThrAsnPheAspIleSerArgTyrAspValGlu 46
œ ·	426 LeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGluAlaTyrAspValAlaAla 445 
œ ·	406 ArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgValAlaGlyAsnLysAsp 425 
σ.	386 HisleuargarglysSerSerGlyPheSerargGlyAlaSerIleTyrArgGlyValThr 405 
α.	366 GluasnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArgGlnGluTyrValAla 385 
α	346 AlaTyrAspLeuAlaAlaLeuLysTyrTrpGlyProSerThrHisIleAsnPheSerIle 365 
œ 	26 Thrarglysglyargglnvaltyrleuglyglytyraspmetgluglulysalaalaarg 345 
	06 ArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCysLysGluGlyGln 325 
ω	286 ArgLysserIleAspThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgHis 305 
ω	s 285   T 107
Φ	GlyThrAspSerValAlaVal 268 
	258 ThrAlaProSer
	erLeuSerLeuSerMetSerProGlySerGinSerSerCysval 25
	erLeuGlySerValGly 23
	12 GGA
	98 GlyLeuLysAsnTrpValAlaProThrArgGluPheSerThrHisGlnGlnValLeuGlu 2
	ysGluThrHisValSerAspCysSer ::: AGAAATTACGGGAATGAC
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US-10-024-632-2 (1-663) x US-10-059  1 MetLysArgIleAsnGluSer	Alignment Scores: 9.4e-133 Score: 1322.00 Percent Similarity: 52.70% Best Local Similarity: 43.13% Query Match: 37.75% DB:	RESULT 8 US-10-059-911-39 ; Sequence 39, Application US/10059911 ; publication No. US20030159180A1 ; publication No. US20030159180A1 ; publication No. US20030159180A1 ; publication No. US20030159180A1 ; publication No. US20030159180A1 ; publication No. No. Inc. ; publication No. No. Inc. ; publication No. No. Inc. ; publication No. No. Inc. ; publication No. Inc. ;	Qy 663 Thr 663 Db 1931 TCT 1933	Qy 643 MetArgProSerProAlaile	Oy 624 IleValAsmProIleGly ::: ::: :::     Db 1814 ATGTTCGGATCAAATATGGGC	Qy 606 ProGluLysArgGlyProSerLe	Qy 586 ThrHisPheSerAsnThrSer	Db 1720	1709	· 6	Db 1700	1697 GAA	
59-911-39 (1-1668) erAsnAsnThrAspAspGlyAsnAsnHisAsnTrpLeuGly 20 :::::::	Length: 1668 Matches: 311 Conservative: 69 Mismatches: 117 Indels: 224 Gaps: 21	University of California r Altering Organ Mass in Plants 10/059,911 17 of Artificial Sequence:truncated or ToDNA transgene ANTMRII, temperature mutant		roSerProAlaIleSerLeuSerHisLeuProValPheAlaSerTrpThrAsp 662 	IleValAsnProIleGlyThrSerValThrSerTrpLeuProSerProThrValGln 642	ProGluLysArgGlyProSerLeuLeuPheProMetProProMetGluThrLys 623	xSerLeuValThrSerLeuSerSerSerArgGluAlaSer 605 		GCTCTPAARGCT 1720	ArgAsnSerAlaPheSerMetAlaLeuGlnAspLeuIle 565	  GACCAPACC 17	ordindindinalaAsndivAsndivSerAspdinivs 545	LysMet 525

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663 TOT 1665	CTTAAGACCGTCGCTCTTACTTTGCCTCAGATGCCGGTTTTCGCTGCTTGGGCTGAT	624 IleValAshbrolleGlyThnSerValThnSerTipLeUrToSerFronintvalcin 642	ProGluLysArgGlyProSerLeuLeuPheProMetProProMetGluThrLys	586 ThrHisPheSerAsnThrSerSerLeuValThrSerLeuSerSerSerArgGluAlaSer 605	566 GlyIleAspSerValGlySerGlyGlnHisAsnMetLeuAspGluSerSerLysIleGly 585	546 IleMetAsnCysGlyAsnTyrArgAsnSerAlaPheSerMetAlaLeuGlnAspLeuIle 565 :::    1441 GCTCTAAATGCT		GAA	AspProArgAsnLysAspIIeAspTyrAsnLysServalvalInrServalAsnLasnLasnLasnLasnLasnLasnLasnLasnLasnLa	66 Argilemeta laserserashlediena laseryeidiena laargargiysiysaspasii		Leury rieugry ring reservant de la contra del contra de la contra del contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra del la co			g — g	e e=	326 ThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGluGluLysAlaAlaArg 345 

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Qy  446   lelyspheArgGlyAlaAsnAlaValThrAsnPheAspIleSerArgTyrAspValGlu	Qy 326 ThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGluGluLysAlaAlaArg :::	Qy 269 ASpAlalysLysArgClyHisAlaLysLeuGlyGlnLysGlnProValHis	Qy 178 GluThrThrLysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGlu 197 [
LeAsplieSerArgTyrAspVaIG1u	TASEMETGIUGILIYSÄIAAIAARG 345	U = 14-0	rSerLeuMetProGlnMetThrGlu 197

t Similarity: 54.52% local Similarity: 43.50% arch: 37.32% late of the control of	TTION: (1)(1647) STR INFORMATION: CANOLA AINTEGUMENTA (ANT) S9-911-4 11 Scores: 4.22e-131 Length: 1307.00 Matches:	TYPE: DIA ORGANISM: Brassica napus ORGANISM: Brassica napus PEATURE: OTHER INFORMATION: Canola AINTEGUMENTA (ANT) ortholog partial cDNA OTHER INFORMATION: including coding region PEATURE: NAME/KENY: CDS	SECONTI	59911	29C 19A1	624 IleValAsnProIleGlyThrSerValThrSerTrpLeuPro :::	606 ProGluLysArgGlyProSerLeu	1452 586 1453	Qy 546 IleMetAsnCysGlyAsnTyrArgAsnSerAlaPheSerMetAlaLeuGlnAspLeuIle 565  Db 1441 GCTCTAAATGCT 1452  Oy 566 GlyIleAspSerValGlySerGlyGlnHisAsnMetLeuAspGluSerSerLysIleGly 585	526 ValLeuPheAsnHisProSerGlnGlnGlnGlnAlaAsnGlyAsnGlySerAspGlnLys	Db 1429 GAA 1431
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RESULT 11
US-10-059-911-30
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                                                                                                                                                LeuProSerProThrValGlnMetArgProSerProAlaIleSerLeuSerHisLeuPro
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GTTTTCGCTGCGTGGGCTGATTCT 1644
                                                                                                                       ACTACGAACCCTAATGCTGATCTCAAG---ACCGTTTCTCTTACTCTGCCGCAGATGCCG
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Application
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APPLICANT: Fischer, Robert L.

APPLICANT: Fischer, Yukiko

APPLICANT: The Regents of the University of California

ITILE OF INVENTION: Methods for Altering Organ Mass in Plai

FILE REFERENCE: 023070-090730US

CURRENT APPLICATION NUMBER: US/10/059,911

CURRENT FILING DATE: 2002-06-17

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 30

LENGTH: 1359
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Best Local Similarity:
Query Match:
DB:
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US-10-059-911-26
; Sequence 26, Application US/10059911
; Publication No. US20030159180A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Mizukami, Yukiko
; APPLICANT: The Regents of the Univer
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US-10-059-911-26
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CURRENT FILLING DATE: 2002-06-17
CURRENT FILLING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 1422
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                   GlyMetGlyAsnGluArgAsnGlyValSerLeuGlySerValGlyCysGlyGluLeuGln
                                                                                                                                                                                                                                                                                                                ValAlaProThrArgGluPheSerThrHisGlnGlnValLeuGluGlnGlnMetAsnCys
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                                                                                        TTGTGGAGACAAGCGTTGGGTTTGAGACGACGACGACGGCTGCGAAGAAGAGAGG
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                                                           --GlyThrAspSerValAlaValAspAlaLγsLγsArg
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491 AspīleAspTyrAspLysSerValValThrSerValAsnAspGluGluThrValGlnVal 510
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                                                                                                                                                                                                                                      591 ThrSerSerLeuValThrSerLeuSerSerSerArgGluAlaSerProGluLysArgGly 610
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628 IleGlyThrSerValThrSerTrpLeuProSerProThrValGlnMetArgProSerPro 647
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                                                              TTGAGTTTTCCGGCGATTTTCGCGTTGCCTCAAGTTAATCAAAAGATGTTCGGATCAAAT 1314
                                                                                                                ProSerLeu----LeuPheProMetProProMetGluThrLysIleVal---AsnPro 627
                                                                                                                                                                                                                                                                                                                                                                GlySerGlyGlnHisAsnMetLeuAspGluSerSerLysIleGlyThrHisPheSerAsn 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProSerGlnGlnGlnAlaAsnGlyAsnGlySerAspGlnLysIleMetAsnCysGly 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACACACTCTTGTCTGGAGAGTTAGCGCGAAGGAAC------1155
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Best Local Similarity:
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
FULE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 11885
LENGTH: 1231
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Enou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
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ORGANISM: Glycine max
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421 ACCITIAGIACCCAAGAGGAAGCAGCTGAAGCCTATGACATTGCTGCTATTAAATTCAGA
                                 430 ThrPheSerThrGlnGluGluAlaAlaGluAlaTyrAspValAlaAlaIleLysPheArg 449
                                                                                                                                       410 HisGlyArgTrpGlnAlaArgIleGlyArgValAlaGlyAsnLysAspLeuTyrLeuGly 429
                                                                                                                                                                                                                                                                                                                                    370 ValGlnLeuGluGluMetLysAsnMetSerArgGlnGluTyrValAlaHisLeuArgArg 389
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                                                                                                                                                                                                       301 AAAAGCAGCGGATTCTCAAGAGGGGCCTCCATGTACAGAGGAGTAACAAGGCACCACCAA
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                                                                                                      CATGGAAGGTGGCAAGCTCGAATTGGAAGGGTAGCCGGAAACAAAGATCTATATCTTGGA
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Kovalic, David K.
Screen, Steven E
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US-10-424-599-123485
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                                                                                              ; OTHER INFORMATION: US-10-424-599-123485
Percent Similarity:
Best Local Similarity:
                                              Alignment Scores: Pred. No.:
                                                                                                                      APPLICANT: LA ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Chou Yihua
APPLICANT: Chou Yihua
APPLICANT: Chou Yongwei
ITILE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated '
ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-215322)B
FILE REFERENCE: 38-215322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 123485
LENGTH: 1949
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
FEATURE: THE NEW MARTINE TO THE DAT METTRA47 82514C 1
                                                                                                                                                                                                                                                                                                                                                                     Sequence 123485, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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Alignment Scores: 3.57e-112 Length: 1113 Pred. No.: 1129.50 Matches: 245 Score: 62.70\$ Matches: 29 Percent Similarity: 62.70\$ Conservative: 29 Best Local Similarity: 56.06\$ Mismatches: 58 Query Match: 32.25\$ Indels: 105	TYPE: DNA TYPE: DNA ; ORGANISM: Artificial Sequence ; ORGANISM: Artificial Sequence ; PEATURE: OTHER INFORMATION: Description of Artificial Sequence:truncated or ; OTHER INFORMATION: mutated ANT cDNA transgene ANTDNC1 US-10-059-911-32	CURRENT APPLICATION NUMBER: US/10/059,911 CURRENT FILING DATE: 2002-06-17 NUMBER OF SEQ ID NOS: 42 SOPTMARE: Patentin Ver. 2.1 SEQ ID NO 32 SEQ ID NO 32	APPLICANT: Fischer, Robert L.  APPLICANT: Mizukami, Yukiko  APPLICANT: The Regents of the University of California  APPLICANT: The Regents of the University of California  TITLE OF INVENTION: Methods for Altering Organ Mass in Plants	RESULT 15 US-10-05-911-32 ; Sequence 32, Application US/10059911 ; Sequence 30, Explication US/10059911 ; Publication No. US20030159180A1 ; Publication No. US20030159180A1	Qy 648 AlaIleSerLeuSerHisLeuProValPheAlaSerTrpThrAsp 662     :::   :::     :::	Qy 628 IleGlyThrSerValThrSerTzpLeuProSerProThrValGlnMetArgProSerPro 647  Db 1501GCTAACGTGGATTCTTGGGATCTTATCTTCCAATCTCAGGACT 1542	Oy 608 LysargGlyProSerLeuLeuPheProMetProProMetGluThrLysIleValAsnPro 627	Qy 588 PheSerAsnThrSerSerLeuValThrSerLeuSerSerArgGluAlaSerProGlu 607	Qy 576AsnMetLeuAspGluSerSerLysIleGlyThrHis 587 List ::::::         ::	QY 575 575  Db 1267 CCGCCCCAGCACAATGATCCTCAGTGCAGTGATGAGAGTCATAGAACTCAGCCCTTCTC 1326	QY 575 575  Db 1207 TGACGTGGTAATGAACATGGCAAGCAAGAAAACCACCCAAGTAGTGAGCTGGTTCAGCGTCC 1266	QY 575 575  Db 1147 ATATTGCTGCTATTAAATTCAGAGGAGCGAATGCTGCTACCAACTTGACATAACAAGATA 1206	Qy 567 575	QY 566 566  DB 1028 AAGCATTTACACATGACCACCTTCATGGAAGGTGTCAAGCTCGAGATGGTAGAGTGGAAA 1087	OY 562
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35I AlaLeuLysTyrTrpGlyProSerThrHisIleAsnPheSerIleGluAsnTyrGlnVal 370	311 TyrGluAlaHisLeuTrpAspAsnSerCysLysClyGlyGlyGlnThrArgLySGlyArg 330		460 CTTGTGGAGACAAGCGTTGGGTTTGAGACGACGACAATGGCGGCTGCGAAGAAGAAGAGAGG 519 274 GlyHisAlalysLeuglyGlnLysGlnProValHisArgLysSerIleAsp 290 :::	00 CACCAACAAAACCAAAACCAAAACCACCAAAGCCAAAACCACC	243 SerLeuserheuserMetserProGlySerGlnSerSerCysValThrALaProSer 261			83 ThrHisValSerAspCysSerSerLeuMetProGlnMetThrGluGlyLeuLysAsnTrp			127 SerileTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArgAspLeuLeuSerGln 146    :::::      :::	109 AlaThrMetGlyThrHisGluTyrGlySerHisGluArgGlyLeuSerLeuAsp 126	89 SerGlnThrGlnValMetValProThrSerSerProLysLeuGluAspPheLeuGlyGly 108		14 Gaps: 11 -2 (1-663) x US-10-059-911-32 (1-1113)

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유양

451 AlaAsnAlaValThrAsnPheAspIleSerArgTyrAspValGluArgIle 467

431 PheSerThrGinGluGluAlaAlaGluAlaTyrAspValAlaAlaIleLysPheArgGly 450

411 GlyArgTrpGlnAlaArgIleGlyArgValAlaGlyAsnLysAspLeuTyrLeuGlyThr 430

391 SerSerGlyPheSerArgGlyAlaSerIleTyrArgGlyValThrArgHisHisGlnHis 410

Search completed: March 13, 2004, 11:23:41 Job time : 483 secs

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# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=x1h
-Q=/cg12_1/USPTO_spool/US10024632/runat_09032004_101208_10776/app_query.fasta_1.839
-Q=/cg12_1/USPTO_spool/US10024632/runat_09032004_101208_10776/app_query.fasta_1.839
-DB=EST _QFMY=fastap -SUFFIX=rst -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MAXRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTEXT=pto -NORM=ext +LEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER_US10024632_@CGN 1 1 2135_@runat_09032004_101208_10776 -NCPU=6 -ICPU=3
-NO_MAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LOGILOG
-DEV_TIMEDUT=30 -THREADS=1 -XGAPOP=10 -XGAPOEXT=0.5 -FGAPOP=6
-DEV_TIMEDUT=30 -THREADS=1 -XGAPOP=10 -XGAPOEXT=0.5 -FGAPOP=6
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Delop 6.0 , Delext
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# 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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2942 sa29c04.x	32004 BN40 061	46573 EST6	79292 AZO4.104	74354 sa199102	36846 QCG37g0	UBZ	5492 AU4/5492	F035870 QCG23h0	E800260 sq91c0	K289457 EST75217	K261980 EST7080	Y103852 Zea mays	Q625052 USDA-FP_	U825419 UK108TE	086088 sah35d02	Q122372 EST6079	G790852 sae70g06	647766 NF025G0	A100375 SCVPCL60	232822 SCRUFL30	A189006 SCCCCL4C	F244784 3530_1_5	28154 K017P49P	3041 SCEOHRI	64461 OGC26M12	776 8000	06573 FGAS018	7997 sak40e09	64897 sat04a	780688 sl75e07	00688 se92c0	M094116 sah25f	7326 064803	J188928 BJ1889	267021 EST713	10900 CAbud	3156 sat20d	75882 nad03-	A232734 SCRUFI	109146 Zea ma	30632	127 GM210001	Description

## ALIGNMENTS

	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	AW348127/c	RESULT 1
Bukaryota, Viridiplantae, Streptophyta, Emcryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids, eurosids I, Fabales, Fabaceae; Papilionoideae, Phaseoleae;	Glycine max	Glycine max (soybean)	EST.	AW348127.1 GI:6845837	AW348127	sequence.	GM210001A21A2 Gm-r1021 Glycine max cDNA clone Gm-r1021-4 3', mkNA	AW348127 752 bp mRNA linear EST 04-OCT-2000		

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451

518 571

511

391

331

638

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151

91

271 598

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REFERENCE
AUTHORS
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Query Match:
DB:
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Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Coryell,V

vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Coryell,V

Erpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and Lewin,H.

A Functional Genomics Program for Soybean (NSF 9872565)

Unpublished (1999)

Other_ESTS: A1444013

Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)

Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: (217) 244-6147
Fax: (217) 333-4582
Email: 1-vodkin@uiuc.edu
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                                                                                  IleSerArgTyrAspValGluArgIleMetAlaSerSerAspLeuLeuAlaGlyGluLeu 478
                                                                                                                                       GAAGCATACGATGTAGNNNCGATCAAATTTCGCGGNGCNNNNNGCAGTCACAAACTTTGAC 691
AlaArgArgLysLysAspAsnAspProArgAsnLysAspIleAspTyrAsnLysSerVal 498
                                                ATTTCANNATACGNTGTNNNNNGAATCATNNNNAGTAGCAATCTCCTCGNNGGGGAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Gm_r1021"
//clone lib="Gm_r1021"
//note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
//note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
//note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
//note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
XhoI; Library Gm_r1021 is a sequence-driven, reracked set
of the original library Gm_r1004 which was prepared from
root cDNA. The mRNA was isolated from entire roots of 8
day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's cDNA
Synthesis Kit (catalog #200401) was used to synthesize
the cDNA. The Gm_r1004 library was constructed by Dr.
Paul Keim & Virginia H. Coryell, Department of Biology,
Box5640, Northern Arizona University, Flagstaff, AZ
BOX5640, Northern Arizona University, Flagstaff, AZ
BOX5640, Northern Arizona University, Flagstaff, AZ
BOX1640, paul keim@nau.edu, virginia.coryell@nau.edu.
The contig analysis to select unique genes was performed
by the laboratory of Ernest Retzel, Computational Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center for Comparative and Functional Genom. University of Illinois, http://www.life.uiuc.edu/biotech/keck.html."
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'cultivar="Williams"
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lab_host="XL10-Gold"
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Matches:
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                                                                                                               Centro de Biologia Molecular e Engenharia Genetica Universidade Estadual de Campinas Caixa Postal 6010, 13083-970, Campinas SP, Brazil Tel: 55 19 3788 1039
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information c through the Brazilian Clone Collection Center (BCCC) http://www.bcccenter.fcav.unesp.br
Plate: C06 row: D column: 04
Seg primer: T7 Promoter Primer.
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Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae, PACCAD
Clade; Panicoideae; Andropogoneae; Saccharum.
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599 bp mRNA linear EST 25-SEP-:
SCUFFFL3C06D04.g Saccharum officinarum FL3 Saccharum officinarum
CDNA clone SCUFFL3C06D04 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                             Vettore,A.L., da Silva,F.R., Kemper,E. The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
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            /organism="Saccharum officinarum"
/mol_type="mRNA"
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/clone_lib="Saccharum officinarum FL3"
/note="Organ: Base of developing inflorescence (5cm-long);
/ector: pSport1; Site 1: SalI; Site 2: NotI; An
unidirectional cDNA library generated from (Base of
developing inflorescence (5cm-long)]. cDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
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Zea mays
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Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, Mo 65211 USA
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize CDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hainey.C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V. Maize Mapping Project/DuPont Consensus Sequences for Design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1753)
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CTTGGAGACGAGCAGGGCGCAGTGGAGGAGTCCCCGAGGACGTGGAGGACTTCCTCGGC
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                                                                                                            GTGTGCGGCGAGCTGGGCAGCATCACAGCCAGGTTCTTGCGCCACTACCCGGCGGCGCCA
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                            GCTGGGACGACGGTGGAGAACCCCGGCGGTGACC-
                                                                       ----SerProGlySerGlnSerSerCysValThrAlaProSerGly
                                                                                                                                                  ---CysGlyGluLeuGlnSerLeuSerLeuSerMet--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:638053"
/db_xref="taxon:4577"
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CA232734 558 bp mRNA linear SCRUFL3064D08.g Saccharum officinarum FL3 Saccharum cDNA clone SCRUFL3064D08 5', mRNA sequence.
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                                                                                                                                                                              HisProSerGlnGlnGlnAlaAsnGlyAsnGlySerAsp
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Clone distribution: clone distribution
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Caixa Postal 6010, 13083-970, Camp
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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/clone lib="Saccharum officinarum FL3"
/note="Organ: Base of developing inflorescence (5cm-long);
/note="Organ: Base of developing inflorescence liberated from [Base of unidirectional cDNA library generated from [Base of developing inflorescence (5cm-long)]. cDNA was prepared from polyA+ mRNA using SuperScript plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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1 (dePamphilis,C., Carlson,J., Arrington,J., Zahn,L., Kong,H.,
1 (dePamphiler,M., Landherr,L., Hu,Y., Ilut,D., Wall,K.,
1 (dePamphiler,M., Landherr,L., Hu,Y., Ilut,D., Wall,K.,
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The sequence provided is trimmed of vector and low quality regions.
Pull sequence and original trace file are available from the Plant
Genome Network website (http://pgn.cornell.edu)
Plate: nad03-15ms1 row: h column: 07
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/note="Vector: pBluescript SK (+/-); Site_1: EcoRI;
Site_2: Xho1; Only floral buds with diameter of 2.5 mm of less were used for RNA isolation. This is a directionally cloned, non-normalized library. Avg. insert length: 1134; Primers: M13F and M13R; Antibiotic: 50 ug/ml Ampicillin; Primary Titer: 2E6 pfu total; Amplified Titer: 3.2E10 Primary Titer: 2E6 pfu total; This library has pfu/ml; Mass Excised Titer: 5E10 total; This library has
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been generated by the Floral Genome Project (FGP). The Floral Genome Project is funded by NSF's Plant Genome Research Program (DBI-0115684). More information about the project can be obtained at http://fgp.bio.psu.edu"

R.B.	VEC SO	CA CA DE	מם	γΩ	- DB	γQ	Dio	S S	당 #	Q ¦	B 8	qq	ρ	Ъ	γQ	₽ <b>.</b>	? !	5 5 5	DЬ	Ş	-sn	Alignn Pred. Score Percer Best I Query DB:
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Spermatophyta; Magnoliophyta; rosids; eurosids I; Fabales; Glycine.  1 (bases 1 to 769) Shoemaker, R., Keim, P., Vodkin	GI:260456 ux (soybean) ux viridiplan	5′ 1			CAATCAAA	laI1eLys 	AAAGACCTTTATC	<b>Taki</b> nərdsys	AACAAGGCATC	lThrArgHisH	1A13H1SLEUA             GCTCACTTAA	ATTGAGCÁÁTT	rIleGluAsnT		aArgAlaTyrA	CAAACCAGAA	Clambrard.	HisArgTrpT)             CACAGATGGA	SCÁTÁGGÁÁGT(	LHisArgLysSe	x CD475882	2.11e-78 909.00 96.13% 93.37% 25.96%
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www.resgen.com
Seg primer: -40RP from Gibco
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 {\tt LysLysGluGlyGlnThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGlu}
                                                          G1YVAlThrArgHisArgTrpThrG1yArgTyrG1uAlaHisLeuTrpAspAsnSerCys 320
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                                                                                                                                                                                                                                                  CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                       Goes da Silva,F., Tandolino,A., Lim,H., Baek,J., Jones,K. and Cook,D.
                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vitis vinifera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
                                                                                                                                                               Seq primer: GCCAAACGAATGGTCTAG
Location/Qualifiers
                                                                                                                                                                                                  Email: drcook@ucdavis.edu
                                                                                                                                                                                                                                                                                                       Contact: Douglas
                                                                                                                                                                                                                                                                                                                      Unpublished (2003)
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530 754 6617
         /db xref="taxon:29760" (clone="CAbud0001 IIIR C03" /sex="Hermaphrodite" /dev stage="Pre-bloom (10-11 /lab_host="DH5alpha"
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/mol type="mRNA"
/cultivar="Cabernet Sauvignon
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EST 09-SEP-2003 gnon (Clone 8)

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637 460 577 440

517

457 420

400 397 380 337

days before bloom)"

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TyrAspMetGluGluLysAlaAlaArgAlaTyrAspLeuAlaAlaLeuLysTyrTrpGly
                                                                                                                                                                                                                                                                                                                                                                                                       LysLeuGlyGlnLysGlnProValHisArgLysSerIleAspThrPheGlyGlnArgThr
                                                                                                                                               AspAsnSerCysLysLysGluGlyGlnThrArgLysGlyArgGlnValTyrLeuGlyGly
                                                                                                 GATAATAGTTGCAAGAAGGAGGGGCAGACTAGGAAAGGAAGACAAGTTTATCTGGGGGGG
                                                                                                                                                                                                                                   TCACAATATAGAGGAGTTACAAGGCATAGATGGACTGGTAGATATGAAGCCCATCTTTGG
                                                                                                                                                                                                                                                                                              SerGlnTyrArgGlyValThrArgHisArgTrpThrGlyArgTyrGluAlaHisLeuTrp
                                                                                                                                                                                                                                                                                                                                                             AAGGTTGCACAAAAGCAACCAGTTCATAGGAAGTCCATTGACACATTTGGGCAGAGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ProserGlyThrAspSerValAlaValAspAlaLysLysArgGlyHisAla 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATTGCCATACCCAGATCCCTCCTATGGGGGAGGATGGAATGCCTTGCCTGAAAAACTGG
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SfiI; CABUT is a cNNA library of Vitis vinifera cv.
'Cabernet Sauvignon' Clone & dissected buds. Samples were
collected May 13, 2002 from pre-bloom plants (10-11 days
before bloom), pre-veraison. Sampled vines were located at
the University of Callifornia, Davis, Experimental
Vineyard. cDNAs were made by oligo-dT priming and
directionally cloned: S'and 3' adaptors were used in
cloning as follows:
5'-ANGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
5'-ANGCAGTGGTATCAACGCCAGAGTGGGCCACATG-dT(30)NN-3. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Vitis vinifera cv. cabernet sauvignon (Clone
8) Bud - CABUD"
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맑 8

Best Local Similarity: Query Match:

Percent Similarity:

9.68e~73 855.00 70.63% 59.79% 24.41%

Mismatches: Indels: Conservative: Pred. No.: Alignment Scores:

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REFERENCE
AUTHORS
TITLE
ORIGIN
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CK267021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 TATGATATGGAAGAGAAAGCTGCAAGAGCTTACGATCTGGCGGCCCTCAAATACTGGGGA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA Email: potato-array@tigr.org Clones can be requested from TIGR via potato@tigr.org Seq primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 882)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from abiotic stressed potato tissue Unpublished (2003)
Other ESTs: EST713100
Contact: Robin_Buell
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Solanum tuberosum (potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Solanum tuberosum
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                four separate sets of plants. Set 1 involved saturation of the soil with 150 mm NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 35 C. Heat 12 hr, 1 d, and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 15 hr, 1 d, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="potato about street or EcoRI; Site 2: NotI; /note="Vector: pcWySport6.1; Site 1: EcoRI; Site 2: NotI; supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 grown from streets conditions were applied to C for 3-4 weeks. Abiotic streets conditions were applied to C for 3-4 weeks. Abiotic streets conditions were applied to C for 3-4 weeks. Abiotic streets conditions were applied to C for 3-4 weeks.
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/clone="POAC822"
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/mol_type="mRNA"
/cultivar="Kennebec"
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KEYWORDS
SOURCE
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                                                                                                                                 BJ188928 normalized full length cDNA library, chloronemata, caulonemata and malformed buds Physcomitrella patens subsp.
Physcomitrella patens subsp. Physcomitrella patens subsp.
                                                                                                           cDNA clone pphb45d02 5', mRNA sequence.
                                                                   BJ188928.1 GI:18356869
                                                                                        BJ188928
                                                                                                                                                                                                                                                                       AGCACCAACAACATCAAT 840
                                                                                                                                                                                                                                                                                                                                                                                                    TyrAsnLysSerValValThrSerValAsnAsnGluGluThrValGlnValGlnAlaGly 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuAlaGlyGluLeuAlaArgArgLysLysAspAsnAspProArgAsnLysAspIleAsp 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlnGluGluAlaAlaGluAlaTyrAspValAlaAlaIleLysPheArgGlyAlaAsnAla 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGAGGAAGCAGCGGAAGCGTATGACATTGCAGCCATAAAGTTCAGGGGAGTGAATGCA
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                                                                                                                                                                                                                                                                                                                                                         AGCAATAACAAC---
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                                                       321 LysLysGluGlyGlnThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGlu 340
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A backbone of the vector is basically from pBluescript II (KS),
that was in vivo excised from a 1-FLC phage vector (Carninci et al.
2001). 5' end of the cDNA that was digested with KhoI was ligated
to Sall site of the vector and the 3' end including polyA tail was
ligated to BamHI site of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryophyta; Bryopoida; Funariidae; Funariales; Funariaceae; Physcomitrella. 1 (Dases 1 to 555)
Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H., Nishiyama, T., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kohara,Y. and Hasebe,M. Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Tadasu Shin-i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="normalized full length cDNA chloronemata, caulonemata and malformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/sub_species="patens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:145481"
/clone="pphb45d02"
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Matches:
Conservative:
Mismatches:
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BJ178045
BJ178045.1 GI:18346002
EST.
                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 558)
Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide,H.,
Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y., Shino:
Kohara,Y. and Hasebe,M.
Comparative genomics of Physcomitrella patens gametophytic
transcriptome and Arabidopsis thaliana: implication for la
                                                                                                                                                                                                                                                                                                                                                                                                                        Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryoph
Eryopada; Funariale; Funariales; Funariaceae;
                                                                                                                                                                                                                        Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
Tel: 81-559-81-6856
                                                                                                                                                                                                               Fax: 81-559-81-6855
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riaceae; Physcomitrella.
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     CF807326 748 bp mRNA linear EST 2 psHB023xF07f USDA-IFAFS:Expression of Phytophthora sojae during infection and propagation Phytophthora sojae cDNA sHB023F07 5, mRNA sequence.
                                                                                                                          ArgTyr 462
                                                                                                 CGTTAC
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

COMMENT JOURNAL MEDLINE PUBMED

clone

RESULT 10 BJ178045 LOCUS

DEFINITION

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US-10-024-632-2 (1-663) x BJ178045
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/mol type="mRNA"
/sub species="patens"
/db xref="taxon:145481"
/clone="pphb21g12"
/clone="pphb21g12"
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1 (bases 1 to
Tyler, B.
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BACKWARD: BK reverse primer
Plate: 023 row: F column: 07
Seq primer: BK reverse primer
High quality sequence stop: 748.
Location/Qualifiers
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Contact: Tyler
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Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1880 Pratt Dr., Blacksburg, VA 24061, Tel: 540-231-7318
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                                                                                                                          IleAsnPheSerIleGluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArg 380
                                                    GlnGluTyrValAlaHisLeuArgArgLysSerSerGlyPheSerArgGlyAlaSerIle
                                                                                              ACCAACTTTCCCATCTATGAGAAGGAACTGAGGAGATGATTTAGAGAACATGACCAGG
                                                                                                                                                          garaagecagecagecritacearcreecagerereagiracreegerecaacraecace
                                                                                                                                                                                   GlulysAlaAlaArgAlaTyrAspLeuAlaAlaLeuLysTyrTrpGlyProSerThrHis 360
                                                                                                                                                                                                                          AGAAGAGAAGGCCAAAGCAGGAAAGGAAGACAAGTTTACCTGGGTGGTTATGACAAGGAA
{\tt TyrArgGlyValThrArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgVal}
                                   CAAGAGTTTGTTGCTTCTACGAAGGAAGAAGTTGGTTTCTCTAGGGGGGGCCTCTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 748)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="48 hr. post infection stage"
/lab_host="Soybean plant"
/clone_lib="USDA-IFAFS:Expression of Phytophthora sojae
/clone_stage="USDA-IFAFS: Expression of Phytophthora sojae
genes during infection and propagation"
/note="Yector: pBK-CMV; Site_1: EcoR1; Site_2: Xho1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="mycelium"
/cell_line="P6497"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Phytophthora
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Marrin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Pubbic Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots;

spermarophyta; Magnoliophyta; eddicotyledons; core eddicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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sah25f05.y1 Gm-c1036
ID: Gm-c1036-2554 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com High quality sequence stop: 431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
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/colone_lib="Gen-close"
/clone_lib="Gen-close"
/clone="Vector: pspCRF1; Site 1: NotI, Site 2: SalI; This
/note="Vector: pspCRF1; Site 1: NotI, Site 2: SalI;
/note="Vector: pspCRF1; Site 1: NotI, Site 2: SalI;
/note="Vector: pspCRF1; Site 1: NotI, Site 2: SalI;
cDNA library was constructed from mRNA is to 9 months)
cultured on MSD 20. The library was prepared using the
rife Technologies psuperscript cDNA library construction
kit. Complementary DNA was synthesized from mRNA using a
poly (dT) sequence with a NotI restrictions site. SalI
linkers adapters were ligated to the blunt-ended cDNA
fragments followed by NotI digestion. The cDNA fragments
were directionally cloned into the NotI-SalI restriction
site of the pspCRTI vector. The ligated cDNA fragments
were transformed into E.coli ElectroMax DH10B host cells.
This library was constructed in the laboratory of Dr. Lila
Vodkin by Anu Khanna at the University of Illinois at
                                                                                                                                                                                                                                                                                                                                                                                                             1. .590
| Organism="Glycine max" |
| /organism="Glycine max" |
| /mol type="mRNA" |
| /db xref="taxon:3847" |
| /clone="GENOME SYSTEMS CLONE ID: Gm-c1036-2554" |
| /tissue type="somatic embryos cultured on MSD 20" |
| /lab_host="DH10B" |
| /lab_host="DH10B" |
| /lab_host="DH10B" |
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Glycine max cDNA clone GENOME SYSTEMS CLONE
similar to TR:098YC2 Q98YC2 F11M15.6 PROTEIN.
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Dr. Lila
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                          REFERENCE
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                                                                 EST.

Glycine max (soybean)

Glycine max

Glycine max

Bukaryota; Viridiplantse; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantse; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magmoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magmoliophyta; Fabaceae; Papilionoideae; Phaseoleae;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                               AW200688 644 bp mRNA linear EST 02-DEC-2001 se92c07.yl Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-229 5' similar to TR:Q41832 Q41832 OPEN READING FRAME. ;;
1 (bases 1 to 644)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
                                                                                                                                                                                                                                                       AW200688.1
                                                                                                                                                                                                                                                                                               mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrGluAlaHisLeuTrpAspAsnSerCysLysGluGlyGlnThrArgLysGlyArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaLeuLysTyrTrpGlyProSerThrHisIleAsnPheSerIleGluAsnTyrGlnVal 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerAsnLeu---LeuAlaGlyGluLeuAlaArgArgLysLysAsp 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaAsnAlaValThrAsnPheAspIleSerArgTyrAspValGluArgIleMetAlaSer 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyArgTrpGlnAlaArgIleGlyArgValAlaGlyAsnLy8AspLeuTyrLeuGlyThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCACTGAAGTACTGGGGGACATCCACCACTACCAACTTTCCAATTAGTAACTATGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                               AACACTCTCCCAATAGGAGGAGGAGCTGCAAAGCGTCTGAAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCAGTGGTTTCTCCAGGGGTGCATCAATGTATCGTGGAGTTACAAGGCATCACCAACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.26e-71
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Gaps:
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Best Local Similarity:
Query Match:
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                                                            281 LysGlnProValHisArgLysSerIleAspThrPheGlyGlnArgThrSerGlnTyrArg 300
                             CAGAAACCCTCTCCAAAGAAAACCGTCGACACCTTCGGCCAACGCACCTCCATCTACCGC
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S 닭 8

2.82e-68 807.00 92.61% 84.09% 23.04%

Length:
Matches:
Conservative:

148 13 0

(1-644)

173

Gaps: Mismatches: Indels: Ş 맑 S 밁 S 밁 Ś 밁 Ş 밁 S 片 Ś

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Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35601 For further in
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 968 Std Error: 0.00
High quality sequence stop: 418.
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Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
M444 Forest Park Parkway, Box 8501, St. Louis, MO 63
/clone lib="Gm-cl027"
/clone = Typector: pBluescript II SX+; Site 1: EcoNI; Site 2: XhoI; This cDNA library was constructed—from mRNA isolated from cotyledons of 3 - and 7-day-old williams seedlings which were propagated on paper towels with distilled water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal amounts of mRNA was used for cDNA synthesis. Stratagene's cDNA Synthesix Kit (catalog number 200401) was used to synthesize the cDNA. First- stranded synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's cDNA synthesize trand synthesis primer was used. An anchor nucleotide (V=A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGACATGACTGCAGG(T)] 18] to anchor the primer at the 5' end of the poly(A) tract. After second- strand synthesis, the cDNA ends were filled in with cloned pen LDNA, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI, all XhoI sites in the cDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBRI Life Tecknologies' cDNA size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript (tm) II XR Predigested vector (pBluescript IS(+)) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). 97% of the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=30). This library was constructed by Dr. Paul Keim and Dr. Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Glycine max"

/mol type="mRNA"

/db_xref="teaxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1027-229"

/tissue_type="cotyledons of 3- and 7-day-old Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seedlings"
/lab_host="DH10B"
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 500)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW780688.1 GI:7795291
EST.
Glycine max (soybean)
Glycine max
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                                                                                                                                Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 412.
                                                                                                                                                                                                                                                                                           Confract: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATGACATTGCTGCTATCAAATTCAGGCGATTAAATGCAGTCACAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGGAAACAAAGACCTCTACCTTGGAACTTTCAGCACCCAAGAAGAAGCTGCTGANGCC 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGAGTTTGTTGCTTCTACGAAGGAAGGAAGCAGTGGTTTCTCTAGGGGGGCCTCTATA 473
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/clone="genome_systems_clone_id: Gm-c1027-7165"
                                                                                                               Location/Qualifiers
                                                                 organism="Glycine max"
                                                                                                                                                                                                                                                                                               Louis, MO 63108, USA
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seedlings"
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/lab_host="DH10B"
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οy	망	Ş	Дb	Qy	Dβ	<i>Q</i>	дb	Qy	Дb	γQ	Дb	δ	US-10-024-632-2	DB:	Query Mat	Best Local Similar:	Score:	Pred. No.:
414	303	394	243	374	183	354	123	334	63	314	ω	294	-632		<u>с</u>	l Sir		••
GlnAlaArgI	TTCTCTAGGG	PheSerArgG	GAGATGAAGA	GluMetLysA	TACTGGGGTC	TyrTrpGlyP	CTGGGTGGTT	LeuGlyGlyT	CATCTATGGG	HisLeuTrpA	GAGCGCACCT	GlnArgThrS	(1-663)			tv:		
leGlyArgVal	GGGCCTCTATA	lyAlaSerIle	ACATGACCAGG	snMetSerArg	CAACTACCACC	roSerThrHis	ATGACAAGGAA	yrAspMetGlu	ACAATAGTTGT	spAsnSerCys:	CCATCTACCGC	erGlnTyrArg	x AW780688	10	22.62%	87.35%	792.00	5.33e-67
AlaGlyAsnLysAspLeu	TACAGAGGAGTGACGAGA	TyrargGlyValThrarg	CAAGAGTTTGTTGCTTCT	GlnGluTyrValAlaHis 	ACCAACTTTCCCATTTCC	IleAsnPheSerIleGlu	GATAAGGCAGCCAGGGCT	GluLysAlaAlaArgAla :::	AGAAGAGGCCAAAGC	LysLysGluGlyGlnThr	GGCGTCACCCGACATAGA	GlyValThrArgHisArg	(1-500)	Gарв:	Indels:	Mismatches:	Matches:	Length:
GlnAlaArgIleGlyArgValAlaGlyAsnLysAspLeuTyrLeuGlyThrPheSerThr	TTCTCTAGGGGGGCCTCTATATACAGAGGAGTGACGAGACACCAGCATGGCCGATGG	PheSerArgGlyAlaSerIleTyrArgGlyValThrArgHisHisGlnHisGlyArgTrp	GAGATGAAGAACATGACCAGGCAAGAGTTTGTTGCTTCTCTACGAAGGAAG	GluMetLysAsnMetSerArgGlnGluTyrValAlaHisLeuArgArgLysSerSerGly	TACTGGGGTCCAACTACCACCACCAACTTTCCCATTTCCAACTATGAGAAGGAACTGGAG	TyrTrpGlyProSerThrHisIleAsnPheSerIleGluAsnTyrGlnValGlnLeuGlu	CTGGGTTGGTTATGACAAGGAAGATAAGGCAGCCAGGGCTTACGATCTCGCAGCTCTCAAG	LeuGlyGlyTyrAspMetGluGluLysAlaAlaArgAlaTyrAspLeuAlaAlaLeuLys	CATCTATGGGACAATAGTTGTAGAAGAGAAGGCCAAAGCAGGAAAGGAAGACAAGTTTAC	HisLeuTrpAspAsnSerCysLysLysGluGlyGlnThrArgLysGlyArgGlnValTyr	GAGCGCACCTCCATCTACCGCGGCGTCACCCGACATAGATGGACGGGAAGATACGAAGCT	GlnArgThrSerGlnTyrArgGlyValThrArgHisArgTrpThrGlyArgTyrGluAla		0	O,	0 H	130	500
433	362	413	302	393	242	373	182	353	122	333	62	313						

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REFERENCE
AUTHORS
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Kucaba,T., Martin,J.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Pape,D., Harvey,N.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
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Sat04a07.yl Gm-c1036 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1036-12685 5' similar to TR:Q9SYC2 Q9SYC2 F11M15.6 PROTEIN. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BU964897.1 GI:24205644
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Seq primër: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop: 445.
Location/Qualifiers
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/clone="SOYBEAN (CONE ID: Gm-c1036-12685"
/tlssue_type="somatic embryos cultured on MSD 20"
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שמ	γ	Db Db	νQ	Дb	Ş	В	δ	qq	γQ	90	Ş	Db	Ş	дb	Q	ф	γQ	дb	Qy	US-10-0	Alignment Pred. No. Score: Percent S Best Loca Query Mat DB:
543 AAGCGT 548	480 ArgArg 481	483 CGCTACGACGTGAAAGCCATCCTTGAAAGC	tAlaS	423 TACGACATAGCTGCGATAAAGTTCAGAGGTCTCAACGCTGTCACAAACTTTGACATGAG	441 TyrAspValAlaAlaIleLysPheArgGly	363 GCAGGAAACAAAGATCTTTACTTGGGAACTTTCAGTACTGAAGAAGAGGCTGCTGAAG	421 AlaGlyAsnLysAspLeuTyrLeuGlyThr	303 TATCGTGGAGTTACAAGGCATCACCAACAC	401 TyrArgGlyValThrArgHisHisGlnHisGlyArgTrpGlnAlaArgTleGlyArgVal	243 CAAGAATTTGTTGCTGCCATTAGAAGGAAA	381 GlnGluTyrValAlaHisLeuArgArgLys	AAG	361 IleAsnPheSerIleGluAsnTyrGlnVal	123 GAAAAAGCAGCTAGGTCTTATGATTTAGCTGCACTGAAGTACTGGGGGACATCCACCACT	341 GluLysAlaAlaArgAlaTyrAspLeuAlaAlaLeuLysTyrTrpGlyProSerThrHis	63 AGAAGGGAAGGCAATCAAGAAAAAGGACGCCAAGTTTATTTGGGTGGATATGATAAAGAA	ysLysGluGlyGlr	3 GGAGTAACGCGACATAGATGGACTGGAAGGTATGAAGCTCACCTTTGGGATAATAGCTG	301 GlyValThrArgHisArgTrpThrGlyArg	)24-632-2 (1-663) x BU964897 (1-552)	nt Scores: 0.: 790.50 Similarity: 91.21% cal Similarity: 80.22% atch: 13
		CGCTACGACGTGAAAGCCATCCTTGAAAGCAACACTCTCCCCAATAGGAGGAGGAGGAGCTGCA 542	erSerAsnLeuLeuAlaGlyGluLeuAla 479	CTCAACGCTGTCACAAACTTTGACATGAGC 482	TyrAspValAlaAlaIleLysPheArgGlyAlaAsnAlaValThrAsnPheAspIleSer 460	Trcagracionada de decrecto de la comercia del comercia del comercia de la comercia del la comercia del la comercia de la comercia de la comercia de la comercia de la comercia de la comercia de la comercia de la comercia de la comercia de la comercia de la comer	aGlyAsnLysAspLeuTyrLeuGlyThrPheSerThrGlnGluGluAlaAlaGluAla 440	TATCGTGGAGTTACAAGGCATCACCAACACGGAAGATGGCAAGCAA	GlyArgTrpGlnAlaArgIleGlyArgVal 420 	CAAGAATTTGTTGCTGCCATTAGAAGGAAAAGCAGTGGTTTCTCCAGGGGTGCATCAATG 302	GlnGluTyrValAlaHisLeuArgArgLysSerSerGlyPheSerArgGlyAlaSerIle 400	GAATTGGATGAAATGAACACATGACGCGA 242	leAsnPheSerIleGluAsnTyrGlnValGlnLeuGluGluMetLysAsnMetSerArg 380	GCACTGAAGTACTGGGGGACATCCACCACT 182	AlaLeuLysTyrTrpGlyProSerThrHis 360	CAAGTTTATTTGGGTGGATATGATAAAGAA 122	GlnValTyrLeuGlyGlyTyrAspMetGlu 340	TATGAAGCTCACCTTTGGGATAATAGCTGT 62	hrArgHisArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCys 320		Length: 552 Matches: 146 Conservative: 20 Mismatches: 15 Indels: 1 Gaps: 1

Search completed: March 13, 2004, 07:59:35 Job time : 2990 secs

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Re
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          809742 seqs, 211153259 residues
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3502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA: *
                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (without alignments)
3684.069 Million cell updates/sec
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esult No.	Score	% Query Match Length DB	ength	80	ID	on	
1	3502	100.0	663	13	US-10-024-632-2	Sequence 2, Appli	
N	1715	49.0	665	ü	US-10-024-632-4	Sequence 4, Appli	
Lυ	1408.5	40.2	642	13	US-10-024-632-6	Sequence 6, Appli	
4.	1349.5	38.5	669	13	US-10-024-632-9	Sequence 9, Appli	
ເກ	1328	37.9	555	14	US-10-059-911-2	Sequence 2, Appli	
თ	1319	37.7	555	14	US-10-059-911-21	Sequence 21, Appl	
7	1313	37.5	555	14	US-10-059-911-22	Sequence 22, Appl	
00	1307	37.3	548	14	US-10-059-911-5	Sequence 5, Appli	
9	1233.5	35.2	452	4	US-10-059-911-13	Sequence 13, Appl	
10	1224	35.0	473	<u>1</u> 4	US-10-059-911-9	Sequence 9, Appli	
11	1180.5	33.7	585	L	US-10-024-632-11	Sequence 11, Appl	
12	1129.5	32.3	370	14	US-10-059-911-15	Sequence 15, Appl	
13	1042	29.8	308	14	US-10-059-911-10	Sequence 10, Appl	
14	955.5	27.3	277	14	US-10-059-911-11	Sequence 11, Appl	
15	948	27.1	574	15	US-10-374-780A-334	Sequence 334, App	

4. U	44	<b>4</b> ω	42	41	40	39	38	37	36	S	34	ω	32	31	30	29	28	27	26	25 55	24	23	22	21	20	19	18	17	16	
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-10-278-536-8	-09-934-455	-10-094-458A-	-10-059-911	-10-059-91	-10-374-780A-131	-10-374-78	-10-024-632-13	-10-374-780A-174	4-780A-13	-10-374-780A-131	-10-059-91	-10-374-780A-2	-10-225-067-140	-10-374-78	-10-094-458A-	-10-374-780	-10-295-403-	-10-094-458A-	-10-286-264-1	-09-	-10-374-780A	-10-059-911-1	-10-059-911-	-10-059-911-2	-10-374-780A-34	-10-374-78	-10-374-780A-40	-10-059-911-	-10-059-911-	
equence 8	equence 42,	equence 8,	equence 24,	equence 12, App	equence 131	equence 1312, A	equence 13, App	equerice 1743; A	quence 1313	equence 1314, A	equence 16	equence 21	equence 14	equence 1311, A	equence 3,	equence 20	equence 34	equence 6,	equence 10	equence	equence 1765, A	equence 14,	equence 19,	equence 23,	equence 346, Ap	equence 2496	equence 400, Ap	equence 25,	equence 17,	

## ALIGNMENTS

RESULT 1 US-10-024-632-2

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Best Local Similarity
                121 RGLGLDSIYYNSQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETT 180
121 RGLSLDSIYYNSQNÁEAQPNRDLLSQPFRQQGHMSVQTHFYYSGLACHGLYQAPLEEETT 180
                                            61 ENGNEHSPITVMPLKSDGSLCILEALKRSQTQVMVPTSSPKLEDELGGATWGTHEYGSHE 120
                                                          61 ENGNFHSPLTVMPLKSDGSLCILEALKRSQTQVMVPTSSPKLEDFLGGATMGTHEYGSHE 120
                                                                                                             1 MKRINESNNTDDGNNHNWLGFSLSPHMKMEATSAATVPTTFYMSPSQSHLSNFGMCYGVG
                                                                                            1 MKRINESNNTDDGNNHNWLGFSLSPHMKMEATSAATVPTTFYMSPSQSHLSNFGMCYGVG
                                                                                                                                          100.0%; Score 3502; milarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
                                                                                                                                                                   DB 13; Length 663;
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APPLICANT: Monsanto Technology LLC
APPLICANT: He, Steve S.
APPLICANT: Dotson, Stanton B.
APPLICANT: Dotson, Stanton B.
TITLE OF INVENTION: WICKLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL
TITLE OF INVENTION: GROWTH AND USES THEREOF
FILE REFERENCE: 38-21(51837)B
CURRENT APPLICATION NUMBER: US/10/024,632
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,896
PRIOR APPLICATION NUMBER: US 60/257,896
PRIOR APPLICATION NUMBER: US 60/257,896
PRIOR APPLICATION NUMBER: US 60/257,896
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEG ID NOS: 33
SOFTWARE: Patentin version 3.1
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Matches 379;
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                                                                                                MKRINESNNTDDGNNHNWIGFSLSPHM-----KMEATSAATVPTTFYMSPSQSHLSN 52
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                                      rgmcygv-gengnfhspitympikspgsicijealkrsgtgymyptsspkiedfiggaim 111
                                                                      MKSMENDDNADLNNQNNWLGFSLSPQMHNIGVSSHSQPSSAAEVVPTSFYHHTAP--LSS 58
          YGFYYGLEAENVGLYSALPIMPLKSDGSLYGLETLSRSQAQAMATTSTPKLENFLGGEAM
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              118
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Publication No. US20020170093A1

REMERAL INFORMATION:

APPLICANT: Homesanto Technology LLC

APPLICANT: He, Steve S.

APPLICANT: Dotson, Stanton B.

APPLICANT: Dotson, Stanton B.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WIT

TITLE OF INVENTION: GROWTH AND USES THEREOF

FILE REFERENCE: 38-21(51,837)B

CURRENT APPLICATION NUMBER: US/10/024,632

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: US 60/257,896

PRIOR APPLICATION NUMBER: US 60/257,896

PRIOR FILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin version 3.1

SEQ ID NO 6
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; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-024-632-6
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US-10-024-632-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 QVIEQQMNCGMGNERNGV--SIGSVGCGELQSISISMSPGSQSSCVT----APSGTDSV
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 42
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                                'n
                                                                                                     40.2%; Score 1408.5; DB 13; Length 642; Similarity 46.5%; Pred. No. 1.1e-122; 141; Conservative 64; Mismatches 149; Indels 179;
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                                                            GNNHNWLGFSLSPHMMEATSAATVPTT------
 YMSPSQSHL-
                                  GGSSNWLGFSLSPHMPAMEVPSSSEPSTAAHHHHHHHPPAAAAAAAGAMSSPPDSATTCNF
   SNFGMCYGVGEN--GNFHSPLTVMPLKSDGSLCILEALKRSQTQ 92
                                                                                                                                      DB 13; Length 642
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US-10-024-632-9
                                                ; TYPE: PRT
; ORGANISM: Oryza
US-10-024-632-9
                                                                                                          APPLICANT: Dotson, Stanton B.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: GROWTH AND USES THEREOF
FILE REFERENCE: 38-21(51837)B
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,896
PRIOR APPLICATION WOMBER: US 60/257,896
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/10024632
Publication No. US20020170093A1
GENERAL INFORMATION:
APPLICANT: Monsanto Technology LLC
APPLICANT: He, Steve S.
Query Match
Best Local Similarity
                                                                                                   ENGTH: 669
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Score 1349.5; DB 13; Pred. No. 4e-117;
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                Sequence 2, Application US/10059911
; Sequence 2, Application US20030159180A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
APPLICANT: THE REGENTS OF Altering Organ Mass in Plants
TITLE OF INVENTION: Methods for Altering Organ Mass in Plants
; TILE REFERENCE: 023070-090730US
; CURRENT APPLICATION NUMBER: US/10/059,911
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO
; TYPE: PRT
CREMITED: Archifornia thaliana
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US-10-059-911-2
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         ORGANISM: Arabidopsis thaliana
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US-10-059-911-2
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US-10-059-911-21
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Best Local
Sequence 21, Application US/10059911
Publication No. US20030159180A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
APPLICANT: Methods for Altering Organ Mass in F
FILE REFERENCE: 023070-090730US
CURRENT APPLICATION NUMBER: US/10/059,911
CURRENT FILING DATE: 2002-06-17
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llarity 43.5%;
Conservative 6
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Pred. No. 3.1e-115;
9; Mismatches 113;
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US-10-059-911-22
// Sequence 22, Application US/10059911
// Publication No. US20030159180A1
// GENERAL INFORMATION:

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SOFTWARE: PatentIn Ver
SEQ ID NO 21
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Best Local Similarity
Matches 312; Conserv
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ORGANISM: Artificial Sequence
FEATURE:
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                                                SPEKRGPSL--LFPMPPMETKIV-NPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWT
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Pred. No. 2.2e-114;
0; Mismatches 114;
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APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
ITITE OF INVENTION: Methods for Altering Organ Mass in Plan
ITITE OF INVENTION: Methods for Altering Organ Mass in Plan
ITITE OF INVENTION: MUMBER: US/10/059,911
CURRENT APPLICATION NUMBER: US/10/059,911
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 555
TYPE: PRT
ORGANISM: Artificial Sequence
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OTHER INFORMATION: Description of Artificial Sequence:structurally
OTHER INFORMATION: altered ANT protein ANTMRII, temperature sensiti
OTHER INFORMATION: mutant
US-10-059-911-22
                                                                                                                                                 545 KIMNCGNYRNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREA 604
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                            SPEKRGPSL--LFPMPPMETKIV-NPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWT 661
                                                                                                                                                                                                                                    NDPRNKDIDYNKSVVTSVNNEETVQVQAGNINNENDSEWKMVLFNHPSQQQQANGNGSDQ
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Pred. No. 7.9e-114;
70; Mismatches 115;
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Sequence 5, Application US/10059911

GENERAL INFORMATION:

APPLICANT: Fischer, Robert L.

APPLICANT: Mischer, Robert L.

APPLICANT: Mischer, Yukiko

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Methods for Altering Organ Mass in Plan

FILE REFERENCE: 023070-090730US

CURRENT APPLICATION UNMER: US/10/059,911

CURRENT FILING DATE: 2002-06-17

NUMBER OF SEQ ID NOS: 42

SOFTMARE: PatentIN Ver. 2.1

SEQ ID NO 5

LENGTH: 548

TYPE: PAT

ORGANISM: Brassica napus

FEATURE:

FEATURE:

FEATURE:

OTHER INFORMATION: Canola AINTEGUMENTA (ANT)

US-10-059-911-5
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US-10-059-911-5
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSNLAAREMYSOMSVMPLRSDGSLCLMEALNRSSHSNNHHHSOV----SSPXMEDF----
                                                                                                                                                                                        AYDVAAIKERGANAVTNEDISRYDVERTMASSNLLAGELARRKKUNDPRNKDIDYNKSVV
                                                                                                                                                                                                                                          RQEYVAHLRRKTSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQBEAAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERNGVSLGSVGCGEL-QSLSLSMSPGSQSSCVTA---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHGLYQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLEQQMNCGMGN 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - FGTHHHNTSHKEAMDLSLDSLFYNTTHA---PNNNTNFQEF----FSFPQTRNHH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVG-ENGNFHSPLTVMPLKSDGSLCILEALKRS-----QTQVMVPTSSPKLEDFLGGA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DUDDSNTTNLLGFSLSSNMLKMGGGEALYSSSSSVATS--SVPPQLVVGDNSSNYGVCY
                                                                            RNISDEEAALTAVVNGGSNKEV----
                                                                                                                   TSVNNEE---TVQVQAGNNNNENDSEWKMVLFNHPSQQQQANGNGSDQKIMNCGNYRNSA
                                                                                                                                                            AYDVAAIKPRGTNAVTNFDITRYDVDRIMASNTLLSGEMARRNS---
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617 MPPMETKI--VNPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWTDT 663
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502 LPQVGPKMFGANVVG-NMSSWTTNPNADLK-TVSLTLPQMPVFAAWADS 548

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; OTHER INFORMATION: Description of Artificial Sequence:structurally; OTHER INFORMATION: altered ANT protein ANTDC1 US-10-059-911-13
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US-10-059-911-13
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                                                                                                   HRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFS 364
                                                                                                                                                                                      DELGGATMGTHEYGSHERG--LSLDSIYYNSQNAEAQPNRDLLSQPF----RQQGHMSVQ 157
                                                                                                                                                                      -----GSFNVGV-----YGEFQQSLSLSMSPGSQSSCITGSHHHQQNQNQNHQSQNH 229
                                                                                                                                                                                                                                    THPYYSGLACHGLYQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQVLE 217
                                                                                                                                                                                                                                                                                                                                            DLYLGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERI 467
                                                                                 DLYLGTFGTQEEAAEAYDVAAIKFRGTNAVTNFDITRYDVDRI 452
                                                                                                                                          79; Indels 127; Gaps
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RESULT 10 US-10-059-911-9 ; Sequence 9, Application US/10059911 ; Publication No. US20030159180A1

RESULT 11
US-10-024-632-11
; Sequence 11, Application US/10024632
; Publication No. US20020170093A1
; GENERAL INFORMATION:

Db Qy	Db Qy	9d 6y	d 4d	Qy Db	dg dg	da Vŷ	Qy dd	QY db	, A	B &	Query Ma Best Loo Matches	GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: ITILE OF IN FILE REFERE CURRENT APPL CURRENT FIL NUMBER OF S SOFTWARE: SOFTWARE: APPLICANT: APPLI
627 PIGTSVTSWLPSPTVQMRPSPNISLSHLPVFAAWTDT 663 :  ::     :  ::     :    :	570 VGSGQHMMLDESSKIGTHFGNISSLVISUSSSKEASPEKKGPSLLFFMFMSIA.V-N 626  403VVEGGSNKEVSTPERLLSFPAIFALPQVNQXWFGS 437	VQAGNNNNENDSEWAMV HENHESQUQQAMANAGSQUATHINGSI TANGSA DIFINAGULATION OF A 40	50 GANAVINEDISRYDVERIMASSNILAGELARRKKONDPRNKDIDYKKSVYTSVNNESTV 	3 4	330 RQVYLGGYDMEEKAARAYDLAALKYWGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRR 389 	273 RGHAKLGOKOPVHRKSIDTFGORTSQYRGVTRHRWTGRYEAHLWDNSCKKEGOTRKG 329 	242 QSLSLSMSPGSQSSCYTAPSGTDSVAVDAKK 272	183 THVSDCSSIMPOMTEGIXNWVAPTREFSTHQQVLEQQMNCGMGNERNGVSLGSVGCGEL- 241 :	127 SIYYNSQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETTKE 182	69 LTWPLKSDGSLCILEALKRSQTQVMVPTSSPKLEDFLGGAIMGTHEYGSHERGLSLD 126	y Match 35.0%; Score 1224; DB 14; Length 473; Local Similarity 44.9%; Pred. No. 1.3e-105; hes 286; Conservative 56; Mismatches 89; Indels 206; Gaps 19;	IL INFORMATION: CCANT: Fischer, Robert L. CCANT: Mizukami, Yukiko CANT: Mizukami, Yukiko CANT: The Regents of the University of California OF INVENTION: Methods for Altering Organ Mass in Plants REFERENCE: 023070-090730US NOT APPLICATION NUMBER: US/10/059,911 NOT FILING DATE: 2002-06-17 NOT SEQ ID NOS: 42 NARE: Patentin Ver. 2.1 NO 9 NARE: Patentin Ver. 2.1 NO 9 NO 9 STH: 473 SI PRT NISM: Artificial Sequence RINFORMATION: Description of Artificial Sequence:structurally SR INFORMATION: altered ANT protein ANTDN1

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APPLICANT: He, Steve S.

APPLICANT: Dotson, Stanton B.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL PROLIFERATION TITLE OF INVENTION: GROWTH AND USES THEREOF FILE REPERENCE: 38-21(51837)B

CURRENT APPLICATION NUMBER: US(10/024,632)

CURRENT FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn version 3.1

SEQ ID NO 11

SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 LEQQMNCGMGNERNGVSLGSVGCGELQSLSLSMSPGSQSSCVTAPSGTDSVA----VDAK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 VQTHPYYSGLACHGLYQAPLEEETTKETHVSDCSSLMPQMTEGLKNWVAPTREFSTHQQV 215
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                                                                                                   DKFGIG-----GDYSHHG-YFSLKGSKYEDGNSETDNSNENR-----
                                                                                                                                              DSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREASPEKRGPSLLFPMPPMETKIVNP 627
                                                                                                                                                                                                 SGEASDELADMYWTA---NSDEQQQHQSTNTNNDASLANSSS-RNSSNPQSPKGSIGLAS 531
                                                                                                                                                                                                                                              AGNININE-NDSEWKMVLFNHPSQQQ-QANGNGSDQKIMNCGNYRNSAFSMALQDLIGI-- 567
                                                                                                                                                                                                                                                                                              SAVTNEDISRYDVKRICSSSTLIGGELAKRSPKDTASIAPEDYN-SCASSASPQPLLAIP 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEBAAEAYDVAAIKFRGA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYLCGYDKEEKAAKAYDLAALKYWGPTTHINFPLSTYEKBLEEMKNMTRQEFVAHLRRKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRPVGKNLTRESVPRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCRKEGQTRKGRQ 296
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41.7%; Pred. No. 2.2e-101;
tive 79; Mismatches 164; Indels 163;
  -LGLVHKIPMFALWNE 585
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RESULT 12 US-10-059-911-15

Sequence 10, Application US/10059911
Publication No. US20030159180A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: Mizukami, Yukiko
INTILE OF INVENTION: Methods for Altering Organ Mass in Plan
FILE REFERENCE: 023070-090730US
CURRENT APPLICATION UNMERS: US/10/059,911
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10

Plants

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APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass in Plants
FILE REFERENCE: 023070-990730US
CURRENT APPLICATION UNUMEER US/10/059,911
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 370
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
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RESULT 13
US-10-059-911-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.3%; Score 1129.5; DB Best Local Similarity 56.4%; Pred. No. 6.5e-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 SIYYNSQNAEAQPNRDLLSQPF----RQQGHMSVQTHPYYSGLACHGLYQAPLEEETTKE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 NYGND-----PSLTHG------YGEFQ 112
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                                                                                                                    GANAVINFDISRYDVERI 467
                                                                                                                                                                                                          KSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFR 449
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                                                                                          GINAVINFDITRYDVDRI 370
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                                                                                                                                                                                                                                                                                                                                                                                              RGH----AKLGQKQPVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSLSLSMSPGSQSSCITGSHHHQQNQNQNHQQSQNHQQISEALVETSVGFETTTMAAAKKK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAAEAYDVAAIKFR
                                                                                                                                                                                                                                                                                                                                                              RGQEDVVVVGQKQIVHRKSIDTFGQRTSQYRGVTRHRWTGRYEAHLWDNSFKKEGHSRKG
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:structurally
OTHER INFORMATION: altered ANT protein ANTON2
US-10-059-911-10
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US-10-059-911-11
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OTHER INFORMATION:
US-10-059-911-11
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Best Local Similarity 54.0
Matches 218; Conservative
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                                                                                                                                         Query Match
Best Local &
                                                                                                                          Matches 198;
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass in |
FILE REFERENCE: 023070-090730US
FULL REPERENCE: 023070-090730US
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 42
SOPTMARE: Patentin Ver. 2.1
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TYPE: PRT
ORGANISM: Artificial Sequence
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IN THE 277
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 VAVDAKKRGH---AKLGOKOPVHRKSIDTFGORTSOYRGVTRHRWTGRYEAHLWDNSCKK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383 YVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYD 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              563 DLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSLSSSREASPEKRGPSL--LFPMPPM 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         503 NNEETVQVQAGNNNNENDSEWKMVLFNHFSQQQQANGNGSDQKIMNCGNYRNSAFSMALQ 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 VAAIKFRGTNAVTNFDITRYDVDRIMSSNTLLSGELARRN------NNSIV--V
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                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETKIV-NPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWTDT 663
WGPSTHINFSIENYQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQ 414
                                                                             RTSQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKY
                                                                                                                          Conservative
                                                                                                                                                                                                                          Description altered ANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.8%; Score 1042; DB 14; 54.0%; Pred. No. 7.7e-89; tive 36; Mismatches 48;
                                                                                                                                           27.3%;
                                                                                                                        ; Score 955.5; DB 1; Pred. No. 8.3e-81; 34; Mismatches 41
                                                                                                                                                                                                                        of Artificial Sequence:structurally protein ANTDN3
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                                                                                                                                                                  DB 14;
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                                                                                                                              Indels
                                                                                                                                                                Length
                                                                                                                                                                     277;
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475 AGELARRKKDNDPRNKDIDYNKSVVTSVNNEETVQVQAGNNNNENDSEWKWVLFNHPSQQ 534
                                               652 SHLPVFASWIDI 663
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                                                                                                                                                                                                                                                                                                                                                                                                                        122 ARIGRVAGNKDLYLGTFGTQEEAAEAYDVAAIKFRGTNAVTNFDITRYDVDRIMSSNTLL
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POMPVFAAWADS 277
                                                                                                    VVEGGSNKEVSTPERLLSFPAIFALPQVNQKMFGSNMGGNMSPWTSNPNAELK-TVALTL
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US-10-374-780A-334
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CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR APPLICATION NUMBER: 60/336,049
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                                                                       SOFTWARE: PatentIn version SEQ ID NO 334
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APPLICANT:
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                                                                                                            PRIOR APPLICATION NUMBER: 10/:
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
                                                                                                                                                                                                                                                                                                                            PRIOR
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: MEI-0047 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sherman, Bradley K
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TYPE: PRT ORGANISM: Arabidopsis thaliana FEATURE:
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                                                       LENGTH: 574
                                                                                                                                                                        FILING
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                                                                                                                                                                                                                                              APPLICATION NUMBER: 10/171,468
FILING DATE: 2002-06-14
                                                                                                                                                                                        APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/338,692
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Dubell III, Arnold T
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Broun, Pierre E
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) OTHER INFORMATION: G1793 (conserved domain in AA coordinates:179-255, 281-349) US-10-374-780A-334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 YEKEVEENKHMTRQEFVAAIRRKSSGFSRGASMYRGVTRHHQHGRWQARIGRVAGNKDLY 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 YQVQLEEMKNMSRQEYVAHLRRKSSGFSRGASIYRGVTRHHQHGRWQARIGRVAGNKDLY 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 TGRYEAHLWDNSCRREGQSRKGRQVYLGGYDKEDKAARSYDLAALKYWGPSTTINFPIIN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 TGRYEAHLWDNSCKKEGQTRKGRQVYLGGYDMEEKAARAYDLAALKYWGBSTHINFSIEN 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 MSPGSQSSCVTAPSGTDSVAVDAKKRGHAKLGQKQPVHRKSIDTFGQRTSQYRGVTRHRW 307
533 E-----PPTVKTDYDMPSSDGTGGYSGWTSESVQ-GSNPG-----GVPTMWNE 574
                                                               608 KRGPSLLFPMPPMETKIVNPIGTSVTSWLPSPTVQMRPSPAISLSHLPVFASWTD 662
                                                                                                                                         482 SNPAL---LHGLVSTSIVDNNNNN----GGSSGSY--NTAAFLGNHGIGIGSSSTVGSTE
                                                                                                                                                                                                                                                                           430 -- ISHYNNNAHDSS----SFNHHSYIQTQLHLHQQTNNYLQQQSSQN--SQQLYNAYLH 481
                                                                                                                                                                                                                                                                                                                                          508 VQVQAGNNNNENDSEWKWVLFNHPSQ-------QQQANGNGSDQKIMNCGNY 552
                                                                                                                                                                                                                                                                                                                                                                                                                371 ALESSKKREAEMIALGSSFQYGGGSSTGSGSTSSRLQLQPYPLSIQQPLEPFLSLQNND- 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485 --NDPRNKDID-----VTSVNNEET 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           428 LGTFSTQEEAAEAYDVAAIKFRGANAVTNFDISRYDVERIMASSNL-LAGELARRKKD-- 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 MGTTAGNNVVDKASPSETTGDNASGGALAVVETATP--RRALDTFGQRTSIYRGVTRHRW 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 CDSNTPNN------SSYHELQESAHN-------------------------------LQSLTLS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 CSSLMPQMTEGLKNWVAPTREFSTHQQVLPQQMNCGMGNERNGVSLGSVGCGELQSLSLS 247
                                                                                                                                                                                                        553 RNSAFSMALQDLIGIDSVGSGQHNMLDESSKIGTHFSNTSSLVTSL----SSSREASPE 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 IYYNSQNAEAQPNRDLLSQPFRQQGHMSVQTHPYYSGLACHGLYQAPLEEETTKETHYSD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 DYYFHTNS-LMP------SVQSN-----SVQSN-----DVVVAA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 -----EGG------EVPKVADPLG--VSKPDENQSNHLVAYNDS 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 PLTVMPLKSDGSLCILEALKRSQTQVMVPTSSPKLEDFLGGATMGTHEYGSHERGLSLDS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 NNHNWLGFSLSPHMKMEATSAATVPTTFYMSPSQSHLSN-----FGMCYGVGENGNFHS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NSNNWLGFPLSPN-----NSSLPPHEYNLGLVSDHWDNPFQTQEWNMINPHGGGGD--- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGTFSTEEEAAEAYDIAAIKFRGLNAVTNFEINRYDVKAILESSTLPIGGGAAKRLKEAO 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 574;
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Search completed: March 9, 2004, 10:52:46 Job time : 40 secs